From:	Switzer, Juliet
Sent:	Monday, October 18, 2004 5:22 PM
To:	Fredman, Jeffrey
Cc:	O'Bryen, Barbara
Subject:	search request

Hi Jeff,

Please approve teh search request for more than 10 sequences. Thanks.

PLEASE FORWARD DIRECTLY TO BARB OBRYEN.

thanks.
Juliet

HI
for 09/701626

please search the following:

1. Please do an oligo search of seq id no 11 in PRIOR ART nuceic acid databases. Please limit hits to sequences of 100 nucleotides or fewer.

2. Please search SEQ ID NO 84 in genbank and genseq databases. please return all 100% hits.

3. Please search seq id no 80, 81, 82, 83, 86, 87, 88, 89, 90, 91 in PRIOR ART databases and return all 100% hits (only 100% necessary).

please return results on disk.

thanks.

Juliet Switzer
Art Unit 1634
phone: 571-272-753
office: Remsen 2D75

From:	Switzer, Juliet
Sent:	Tuesday, October 19, 2004 8:38 AM
To:	Schreiber, David
Subject:	RE: score/length search 09701626

issued and published. not the pending database. thanks

-----Original Message-----
From:	Schreiber, David
Sent:	Tuesday, October 19, 2004 7:04 AM
T :	Switzer, Juliet
Subject:	RE: score/length search 09701626

When you say US patents you mean only issued, correct?

David Schreiber, Ph.D.
Scientific and Technical Information Center
Biotech/Chem Library
Remsen E01A61
571-272-2526

-----Original Message-----
From:	Switzer, Juliet
Sent:	Monday, October 18, 2004 4:55 PM
To:	Schreiber, David
Subject:	FW: score/length search 09701626

David --

Could you please perform a Score/Length sequence search for complements of SEQ ID NO 11, with a minimum hit length of 10 and a maximum hit length of 77, and a score over length cutoff at 70%. ONly do search in US Patents and GenSeq. Thanks.

Please return results on disk. Please give me at least 100 hits and alignments.

Thanks!

Juliet Switzer
Art Unit 1634
phone: 571-272-753
office: Remsen 2D75

1

O'Bryen, Barbara

for 09701626

· seq id no 11, 84, and 85 in all nucleic acid databases. please return results on disk.

thanks.

Juliet

Juliet Switzer
Art Unit 1634
phone: 571-272-753
office: Remsen 2D75
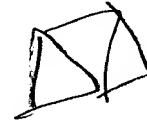
SID 78 - Ann searched results in IFW = free.

SID 79. Ann searched, results in IFW = free

SID 85 - no prior 100% hits → comprising/consisting of SID 85 = genembl - took no prior 100% free of prior art

seq ID No 84 - genembl - need to request more hits.
genseq →

OK issued pats
OK published apps
OK EST

1

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 19:34:52 ; Search time 1269.17 Seconds
                                          (without alignments)
                                          2629.598 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*
                 28: em_un:*

```
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	77	6	BD211287	BD211287 Method of
2	77	100.0	18042	1	AY038186	AY038186 Pseudomon
3	75.4	97.9	77	6	BD211300	BD211300 Method of
4	74.4	96.6	77	6	BD211339	BD211339 Method of
5	74.4	96.6	77	6	BD211344	BD211344 Method of
6	74.4	96.6	14143	6	BD211277	BD211277 Method of
7	74.4	96.6	14143	6	BD211278	BD211278 Method of
8	74.4	96.6	42143	6	BD211280	BD211280 Method of
9	72.8	94.5	77	6	BD211395	BD211395 Method of
10	71.8	93.2	77	6	BD211295	BD211295 Method of
11	71.8	93.2	77	6	BD211331	BD211331 Method of
12	71.8	93.2	77	6	BD211398	BD211398 Method of
13	71.2	92.5	77	6	BD211353	BD211353 Method of
14	70.6	91.7	77	6	BD211317	BD211317 Method of
15	69.8	90.6	77	6	BD211354	BD211354 Method of
16	69.6	90.4	77	6	BD211281	BD211281 Method of
17	69.6	90.4	77	6	BD211298	BD211298 Method of
18	69.2	89.9	74	6	BD211374	BD211374 Method of
19	68.8	89.4	7275	1	AY129393	AY129393 Pseudomon
20	68.6	89.1	77	6	BD211297	BD211297 Method of
21	68.6	89.1	77	6	BD211302	BD211302 Method of
22	68.6	89.1	77	6	BD211316	BD211316 Method of
23	67	87.0	77	6	BD211341	BD211341 Method of
24	66	85.7	77	6	BD211324	BD211324 Method of
25	66	85.7	7300	6	BD211279	BD211279 Method of
26	65.6	85.2	77	6	BD211351	BD211351 Method of
27	64	83.1	78	6	BD211325	BD211325 Method of
28	64	83.1	78	6	BD211327	BD211327 Method of
29	62.4	81.0	78	6	BD211299	BD211299 Method of
30	61.8	80.3	78	6	BD211320	BD211320 Method of
31	61.8	80.3	78	6	BD211405	BD211405 Method of
32	61.8	80.3	78	6	BD211406	BD211406 Method of
33	61.4	79.7	78	6	BD211314	BD211314 Method of
34	61.4	79.7	78	6	BD211323	BD211323 Method of

35	61	79.2	78	6	BD211350	BD211350 Method of
36	60.2	78.2	78	6	BD211335	BD211335 Method of
37	59.8	77.7	78	6	BD211294	BD211294 Method of
38	57.6	74.8	78	6	BD211343	BD211343 Method of
39	56.8	73.8	78	6	BD211315	BD211315 Method of
40	56.8	73.8	5957	1	AY129392	AY129392 Pseudomon
41	56.6	73.5	76	6	BD211288	BD211288 Method of
42	56	72.7	76	6	BD211290	BD211290 Method of
43	56	72.7	76	6	BD211348	BD211348 Method of
44	55.4	71.9	76	6	BD211337	BD211337 Method of
45	55.4	71.9	76	6	BD211349	BD211349 Method of

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 18:33:43 ; Search time 484.569 Seconds
                                              (without alignments)
                                          675.056 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002s:*
                   7: geneseqn2003as:*
                   8: geneseqn2003bs:*
                   9: geneseqn2003cs:*
                   10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	77	3	AAZ44900	Aaz44900 P. alcali
2	75.4	97.9	77	3	AAZ44913	Aaz44913 P. alcali
3	74.4	96.6	77	3	AAZ44952	Aaz44952 P. alcali
4	74.4	96.6	77	3	AAZ44957	Aaz44957 P. alcali
5	74.4	96.6	14143	3	AAZ44981	Aaz44981 P. alcali
6	72.8	94.5	77	3	AAZ44987	Aaz44987 P. alcali
7	72.4	94.0	74	3	AAZ88511	Aaz88511 P. alcali
8	72.4	94.0	74	3	AAZ88515	Aaz88515 P. alcali

9	71.8	93.2	77	3	AAZ44908	Aaz44908 P. alcali
10	71.8	93.2	77	3	AAZ44990	Aaz44990 P. alcali
11	71.8	93.2	77	3	AAZ44944	Aaz44944 P. alcali
12	71.4	92.7	74	3	AAZ88505	Aaz88505 P. alcali
13	71.2	92.5	77	3	AAZ44966	Aaz44966 P. alcali
14	70.6	91.7	77	3	AAZ44930	Aaz44930 P. alcali
15	70.6	91.7	13382	3	AAZ44984	Aaz44984 P. alcali
16	69.8	90.6	74	3	AAZ88516	Aaz88516 P. alcali
17	69.8	90.6	77	3	AAZ44967	Aaz44967 P. alcali
18	69.6	90.4	77	3	AAZ44894	Aaz44894 P. alcali
19	69.6	90.4	77	3	AAZ44911	Aaz44911 P. alcali
20	69.2	89.9	74	3	AAZ88503	Aaz88503 P. alcali
21	68.6	89.1	77	3	AAZ44910	Aaz44910 P. alcali
22	68.6	89.1	77	3	AAZ44915	Aaz44915 P. alcali
23	68.6	89.1	77	3	AAZ44929	Aaz44929 P. alcali
24	67.6	87.8	74	3	AAZ88520	Aaz88520 P. alcali
25	67	87.0	77	3	AAZ44954	Aaz44954 P. alcali
26	66	85.7	77	3	AAZ44937	Aaz44937 P. alcali
27	66	85.7	7300	3	AAZ44982	Aaz44982 P. alcali
28	66	85.7	7300	3	AAZ44983	Aaz44983 P. alcali
29	65.6	85.2	77	3	AAZ44964	Aaz44964 P. alcali
30	64	83.1	78	3	AAZ44938	Aaz44938 P. alcali
31	64	83.1	78	3	AAZ44940	Aaz44940 P. alcali
32	62.4	81.0	73	3	AAZ88521	Aaz88521 P. alcali
33	62.4	81.0	78	3	AAZ44912	Aaz44912 P. alcali
34	61.8	80.3	78	3	AAZ44997	Aaz44997 P. alcali
35	61.8	80.3	78	3	AAZ44933	Aaz44933 P. alcali
36	61.4	79.7	78	3	AAZ44936	Aaz44936 P. alcali
37	61.4	79.7	78	3	AAZ44927	Aaz44927 P. alcali
38	61	79.2	78	3	AAZ44963	Aaz44963 P. alcali
39	60.2	78.2	78	3	AAZ44948	Aaz44948 P. alcali
40	59.8	77.7	75	3	AAZ88508	Aaz88508 P. alcali
41	59.8	77.7	78	3	AAZ44907	Aaz44907 P. alcali
42	58	75.3	74	3	AAZ88509	Aaz88509 P. alcali
43	57.6	74.8	78	3	AAZ44956	Aaz44956 P. alcali
44	56.8	73.8	78	3	AAZ44928	Aaz44928 P. alcali
45	56.6	73.5	75	3	AAZ88514	Aaz88514 P. alcali

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 20:14:57 ; Search time 110.853 Seconds
                                              (without alignments)
                                              385.475 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
   ----
       1   24.4   31.7   576 4   US-09-252-991A-1507   Sequence 1507, Ap
  c   2   24.4   31.7   876 4   US-09-252-991A-1565   Sequence 1565, Ap
       3   24.4   31.7   1512 4   US-09-252-991A-1551   Sequence 1551, Ap
  c   4   24.4   31.7   1677 4   US-09-252-991A-1616   Sequence 1616, Ap
       5   24.2   31.4   3796 2   US-08-762-308-11   Sequence 11, Appl
       6   24.2   31.4   3796 4   US-09-844-634-10   Sequence 10, Appl
  c   7   23.4   30.4 12665 4   US-08-961-527-134   Sequence 134, App
  c   8   23   29.9   1212 4   US-09-134-000C-1452   Sequence 1452, Ap
       9   23   29.9   2124 4   US-09-252-991A-7474   Sequence 7474, Ap
      10   22.6   29.4 50341 1   US-08-247-901C-1   Sequence 1, Appli
      11   22.6   29.4 50341 2   US-09-075-904-1   Sequence 1, Appli
      12   22.6   29.4 52297 3   US-09-426-436-1   Sequence 1, Appli

	13	22.6	29.4	52297	4	US-08-705-557-1	Sequence 1, Appli
	14	22.4	29.1	3870	1	US-08-138-641-1	Sequence 1, Appli
	15	22.4	29.1	3870	1	US-08-138-133-1	Sequence 1, Appli
	16	22.4	29.1	3893	1	US-08-138-641-3	Sequence 3, Appli
	17	22.4	29.1	3893	1	US-08-138-133-3	Sequence 3, Appli
	18	22.4	29.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	19	22.4	29.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	20	22.4	29.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	21	22.4	29.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	22	22.2	28.8	549	4	US-09-252-991A-12922	Sequence 12922, A
c	23	22.2	28.8	774	4	US-09-107-532A-1786	Sequence 1786, Ap
	24	22.2	28.8	1308	4	US-09-252-991A-12869	Sequence 12869, A
c	25	22.2	28.8	1800	1	US-08-260-202A-10	Sequence 10, Appl
c	26	22.2	28.8	1800	1	US-08-017-114-10	Sequence 10, Appl
c	27	22.2	28.8	1800	3	US-08-505-307-10	Sequence 10, Appl
c	28	22.2	28.8	1800	4	US-09-609-151A-10	Sequence 10, Appl
c	29	22.2	28.8	1800	5	PCT-US94-02034-10	Sequence 10, Appl
c	30	22	28.6	1883	4	US-08-216-592A-5	Sequence 5, Appli
c	31	21.8	28.3	1332	4	US-09-328-352-2196	Sequence 2196, Ap
c	32	21.8	28.3	3611	4	US-09-976-594-1109	Sequence 1109, Ap
	33	21.6	28.1	681	4	US-09-489-039A-1853	Sequence 1853, Ap
	34	21.6	28.1	2275	4	US-09-391-104-1	Sequence 1, Appli
	35	21.6	28.1	2427	4	US-09-489-039A-4376	Sequence 4376, Ap
c	36	21.6	28.1	4957	4	US-09-332-041-1	Sequence 1, Appli
	37	21.6	28.1	5107	3	US-08-910-647-3	Sequence 3, Appli
	38	21.6	28.1	5107	4	US-09-620-925-3	Sequence 3, Appli
c	39	21.6	28.1	5351	4	US-09-221-017B-771	Sequence 771, App
	40	21.4	27.8	285	4	US-09-313-294A-6577	Sequence 6577, Ap
	41	21.4	27.8	306	4	US-09-313-294A-7582	Sequence 7582, Ap
c	42	21.4	27.8	642	4	US-09-252-991A-14197	Sequence 14197, A
	43	21.4	27.8	975	4	US-09-489-039A-1662	Sequence 1662, Ap
c	44	21.4	27.8	1128	4	US-09-252-991A-14237	Sequence 14237, A
	45	21.4	27.8	1545	4	US-09-252-991A-14029	Sequence 14029, A

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 21:09:03 ; Search time 441.422 Seconds
                                          (without alignments)
                                          791.600 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description

```
---------------------------------------------------------------------------
c   1    27.6    35.8     514   9   US-09-764-864-389        Sequence 389, App
    2    27.6    35.8     629   9   US-09-764-864-797        Sequence 797, App
    3    27.6    35.8    2874  16   US-10-104-047-1915        Sequence 1915, Ap
    4    27.4    35.6      34  15   US-10-407-637-29         Sequence 29, Appl
c   5    26.4    34.3    1976  13   US-10-282-122A-11824      Sequence 11824, A
c   6    26.2    34.0   46846  13   US-10-087-192-1018        Sequence 1018, Ap
c   7    26      33.8  189158  13   US-10-087-192-415         Sequence 415, App
    8    25.2    32.7     549  13   US-10-027-632-276435      Sequence 276435,
    9    25.2    32.7     549  16   US-10-027-632-276435      Sequence 276435,
   10    24.8    32.2     404   9   US-09-960-352-10885       Sequence 10885, A
   11    24.8    32.2     405   9   US-09-960-352-6906        Sequence 6906, Ap
   12    24.8    32.2     408   9   US-09-960-352-12808       Sequence 12808, A
c  13    24.8    32.2     461   9   US-09-960-352-2605        Sequence 2605, Ap
   14    24.6    31.9    2571  16   US-10-369-493-44175       Sequence 44175, A
c  15    24.4    31.7    1470   9   US-09-815-242-7855        Sequence 7855, Ap
   16    24.4    31.7 9025608  15   US-10-156-761-1           Sequence 1, Appli
   17    24.2    31.4    1530  13   US-10-282-122A-15192      Sequence 15192, A
   18    24.2    31.4    3796  16   US-10-410-012-6           Sequence 6, Appli
c  19    23.8    30.9     262  13   US-10-424-599-87272       Sequence 87272, A
   20    23.8    30.9    1080  16   US-10-369-493-28310       Sequence 28310, A
   21    23.8    30.9    1080  16   US-10-369-493-31068       Sequence 31068, A
c  22    23.6    30.6    6274  10   US-09-822-846-501         Sequence 501, App
c  23    23.4    30.4     805  13   US-10-425-114-27162       Sequence 27162, A
   24    23.4    30.4     979  17   US-10-240-240A-117        Sequence 117, App
c  25    23.4    30.4    1827  10   US-09-769-787-215         Sequence 215, App
   26    23.4    30.4    3606  15   US-10-156-761-2645        Sequence 2645, Ap
c  27    23.4    30.4   12665  13   US-10-158-844-134         Sequence 134, App
c  28    23.4    30.4 9025608  15   US-10-156-761-1           Sequence 1, Appli
c  29    23.2    30.1     281   9   US-09-294-093B-4316       Sequence 4316, Ap
c  30    23.2    30.1     465  13   US-10-027-632-248582      Sequence 248582,
c  31    23.2    30.1     465  16   US-10-027-632-248582      Sequence 248582,
   32    23.2    30.1    1371  16   US-10-369-493-26983       Sequence 26983, A
   33    23.2    30.1    1502  10   US-09-814-353-19064       Sequence 19064, A
   34    23.2    30.1    1548  13   US-10-425-114-16732       Sequence 16732, A
   35    23      29.9     434   9   US-09-783-590-7544        Sequence 7544, Ap
c  36    23      29.9     767  13   US-10-027-632-14404       Sequence 14404, A
c  37    23      29.9     767  13   US-10-027-632-145338      Sequence 145338,
c  38    23      29.9     767  13   US-10-027-632-145339      Sequence 145339,
c  39    23      29.9     767  13   US-10-027-632-145340      Sequence 145340,
c  40    23      29.9     767  16   US-10-027-632-14404       Sequence 14404, A
c  41    23      29.9     767  16   US-10-027-632-145338      Sequence 145338,
c  42    23      29.9     767  16   US-10-027-632-145339      Sequence 145339,
c  43    23      29.9     767  16   US-10-027-632-145340      Sequence 145340,
c  44    23      29.9    1113  13   US-10-282-122A-20769      Sequence 20769, A
c  45    23      29.9    1116   9   US-09-815-242-6680        Sequence 6680, Ap
```

OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 20:21:03 ; Search time 4145.39 Seconds
                                         (without alignments)
                                         554.686 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: em_estba:*
                2: em_esthum:*
                3: em_estin:*
                4: em_estmu:*
                5: em_estov:*
                6: em_estpl:*
                7: em_estro:*
                8: em_htc:*
                9: gb_est1:*
                10: gb_est2:*
                11: gb_htc:*
                12: gb_est3:*
                13: gb_est4:*
                14: gb_est5:*
                15: em_estfun:*
                16: em_estom:*
                17: em_gss_hum:*
                18: em_gss_inv:*
                19: em_gss_pln:*
                20: em_gss_vrt:*
                21: em_gss_fun:*
                22: em_gss_mam:*
                23: em_gss_mus:*
                24: em_gss_pro:*
                25: em_gss_rod:*
                26: em_gss_phg:*
                27: em_gss_vrl:*
                28: gb_gss1:*
                29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	31	40.3	510	29	TA382G08P	AL498114 T. brucei
2	29.6	38.4	786	9	AL524576	AL524576 AL524576
3	27.6	35.8	773	12	BI196699	BI196699 602755312
4	27.6	35.8	844	13	BU860474	BU860474 AGENCOURT
c 5	27.4	35.6	610	10	BE620662	BE620662 601483644
c 6	27.2	35.3	453	9	AA752920	AA752920 97AS0655
7	27.2	35.3	760	28	BH987482	BH987482 oej71a01.
8	27.2	35.3	993	13	BX384033	BX384033 BX384033
9	26.2	34.0	492	29	TA100E09Q	AL459350 T. brucei
c 10	26.2	34.0	537	12	BJ054088	BJ054088 BJ054088
c 11	26.2	34.0	543	29	TA289C09Q	AL486560 T. brucei
c 12	26.2	34.0	547	28	AQ656279	AQ656279 Sheared D
13	26	33.8	663	10	BB653255	BB653255 BB653255
14	26	33.8	669	28	AZ511751	AZ511751 1M0356K22
15	26	33.8	839	14	CD853831	CD853831 DH0AMM22Z
16	26	33.8	897	11	AK014720	AK014720 Mus muscu
17	26	33.8	901	13	BY714219	BY714219 BY714219
18	26	33.8	2341	11	AK080712	AK080712 Mus muscu
c 19	25.8	33.5	561	28	BZ866494	BZ866494 CH240_224
c 20	25.8	33.5	707	28	AZ572117	AZ572117 301PvE04
21	25.6	33.2	205	13	BU653751	BU653751 1112108G0
c 22	25.6	33.2	494	12	BJ091203	BJ091203 BJ091203
c 23	25.6	33.2	600	29	CC766634	CC766634 CH240_132
24	25.6	33.2	757	28	AQ869312	AQ869312 nbeb0034P
c 25	25.6	33.2	840	29	CC486572	CC486572 CH240_316
c 26	25.4	33.0	493	28	BZ871227	BZ871227 CH240_211
c 27	25.4	33.0	621	29	CG854023	CG854023 ZMMBBb035
c 28	25.4	33.0	804	13	BU291210	BU291210 604162085
29	25.2	32.7	681	29	CG299984	CG299984 OGWKL09TV
c 30	25.2	32.7	711	14	CD866637	CD866637 AZO2.103P
31	25.2	32.7	886	29	AG050878	AG050878 Pan trogl
32	25.2	32.7	1005	14	CB951973	CB951973 AGENCOURT
33	25	32.5	407	28	BZ874593	BZ874593 CH240_192
34	25	32.5	587	10	AW556958	AW556958 L0275E05-
35	25	32.5	593	14	CK330209	CK330209 H8200E04-
36	25	32.5	728	13	BQ201391	BQ201391 UI-R-DZ1-
37	25	32.5	747	14	CA510215	CA510215 UI-R-FS0-
c 38	25	32.5	837	12	BI951570	BI951570 HVSMEm000
c 39	25	32.5	852	9	AI069008	AI069008 mgae0005a
c 40	25	32.5	881	29	CC522796	CC522796 CH240_371
41	25	32.5	906	29	CG181239	CG181239 PUFPS71TD
42	25	32.5	1293	28	BZ573096	BZ573096 msh2_2941
c 43	24.8	32.2	126	12	BM223146	BM223146 K0132B06-
c 44	24.8	32.2	139	14	CB882696	CB882696 HL02J23w
45	24.8	32.2	325	9	AA980303	AA980303 ua33b04.r

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OM nucleic - nucleic search, using sw model

Run on: ·   October 22, 2004, 04:50:28 ; Search time 1491 Seconds
                                                (without alignments)
                                                2442.191 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23664849745 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2172512

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB ID   Description
----
       1   77 100.0   77   6 BD211287   BD211287 Method of
       2   69   89.6   77   6 BD211344   BD211344 Method of
       3   67   87.0   77   6 BD211300   BD211300 Method of
       4   67   87.0   77   6 BD211331   BD211331 Method of

5	67	87.0	77	6	BD211339	BD211339 Method of
6	57	74.0	77	6	BD211395	BD211395 Method of
7	57	74.0	78	6	BD211320	BD211320 Method of
8	55	71.4	77	6	BD211353	BD211353 Method of
9	55	71.4	77	6	BD211354	BD211354 Method of
10	55	71.4	78	6	BD211294	BD211294 Method of
11	54	70.1	77	6	BD211295	BD211295 Method of
12	54	70.1	77	6	BD211298	BD211298 Method of
13	54	70.1	77	6	BD211317	BD211317 Method of
14	54	70.1	78	6	BD211405	BD211405 Method of
15	54	70.1	78	6	BD211406	BD211406 Method of
16	52	67.5	77	6	BD211341	BD211341 Method of
17	47	61.0	77	6	BD211297	BD211297 Method of
18	45	58.4	77	6	BD211281	BD211281 Method of
19	45	58.4	77	6	BD211302	BD211302 Method of
20	41	53.2	74	6	BD211374	BD211374 Method of
21	41	53.2	77	6	BD211398	BD211398 Method of
22	41	53.2	78	6	BD211350	BD211350 Method of
23	40	51.9	77	6	BD211351	BD211351 Method of
24	40	51.9	78	6	BD211314	BD211314 Method of
25	40	51.9	78	6	BD211325	BD211325 Method of
26	40	51.9	78	6	BD211335	BD211335 Method of
27	39	50.6	77	6	BD211324	BD211324 Method of
28	39	50.6	78	6	BD211299	BD211299 Method of
29	39	50.6	78	6	BD211323	BD211323 Method of
30	39	50.6	78	6	BD211327	BD211327 Method of
31	38	49.4	64	6	BD211394	BD211394 Method of
32	38	49.4	76	6	BD211348	BD211348 Method of
33	38	49.4	77	6	BD211316	BD211316 Method of
34	37	48.1	52	6	BD211355	BD211355 Method of
35	33	42.9	76	6	BD211288	BD211288 Method of
36	33	42.9	76	6	BD211337	BD211337 Method of
37	29	37.7	88	6	BD211283	BD211283 Method of
38	29	37.7	88	6	BD211326	BD211326 Method of
39	28	36.4	75	6	BD211310	BD211310 Method of
40	28	36.4	76	6	BD211349	BD211349 Method of
41	28	36.4	78	6	BD211343	BD211343 Method of
42	27	35.1	43	6	BD211356	BD211356 Method of
43	26	33.8	76	6	BD211301	BD211301 Method of
44	26	33.8	79	6	BD211328	BD211328 Method of
45	25	32.5	77	6	BD211322	BD211322 Method of

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 04:25:35 ; Search time 240 Seconds
                                              (without alignments)
                                              1684.189 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: OLIGO_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size :   0

Total number of hits satisfying chosen parameters: 4343386

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_23Sep04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002as:*
                   7: geneseqn2002bs:*
                   8: geneseqn2003as:*
                   9: geneseqn2003bs:*
                   10: geneseqn2003cs:*
                   11: geneseqn2003ds:*
                   12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB ID   Description
----
       1   77 100.0   77 3   AAZ44900   Aaz44900 P. alcali
       2   69   89.6   77 3   AAZ44957   Aaz44957 P. alcali
       3   68   88.3   74 3   AAZ88515   Aaz88515 P. alcali
       4   67   87.0   74 3   AAZ88505   Aaz88505 P. alcali
       5   67   87.0   77 3   AAZ44952   Aaz44952 P. alcali
       6   67   87.0   77 3   AAZ44913   Aaz44913 P. alcali

7	67	87.0	77	3	AAZ44944	Aaz44944 P. alcali
8	66	85.7	74	3	AAZ88511	Aaz88511 P. alcali
9	57	74.0	77	3	AAZ44987	Aaz44987 P. alcali
10	57	74.0	78	3	AAZ44933	Aaz44933 P. alcali
11	56	72.7	74	3	AAZ88520	Aaz88520 P. alcali
12	55	71.4	74	3	AAZ88516	Aaz88516 P. alcali
13	55	71.4	77	3	AAZ44967	Aaz44967 P. alcali
14	55	71.4	77	3	AAZ44966	Aaz44966 P. alcali
15	55	71.4	78	3	AAZ44907	Aaz44907 P. alcali
16	54	70.1	77	3	AAZ44908	Aaz44908 P. alcali
17	54	70.1	77	3	AAZ44930	Aaz44930 P. alcali
18	54	70.1	77	3	AAZ44911	Aaz44911 P. alcali
19	54	70.1	78	3	AAZ44997	Aaz44997 P. alcali
20	52	67.5	77	3	AAZ44954	Aaz44954 P. alcali
21	47	61.0	77	3	AAZ44910	Aaz44910 P. alcali
22	45	58.4	77	3	AAZ44894	Aaz44894 P. alcali
23	45	58.4	77	3	AAZ44915	Aaz44915 P. alcali
24	41	53.2	74	3	AAZ88503	Aaz88503 P. alcali
25	41	53.2	77	3	AAZ44990	Aaz44990 P. alcali
26	41	53.2	78	3	AAZ44963	Aaz44963 P. alcali
27	40	51.9	77	3	AAZ44964	Aaz44964 P. alcali
28	40	51.9	78	3	AAZ44948	Aaz44948 P. alcali
29	40	51.9	78	3	AAZ44938	Aaz44938 P. alcali
30	40	51.9	78	3	AAZ44927	Aaz44927 P. alcali
31	39	50.6	75	3	AAZ88508	Aaz88508 P. alcali
32	39	50.6	77	3	AAZ44937	Aaz44937 P. alcali
33	39	50.6	78	3	AAZ44912	Aaz44912 P. alcali
34	39	50.6	78	3	AAZ44936	Aaz44936 P. alcali
35	39	50.6	78	3	AAZ44940	Aaz44940 P. alcali
36	38	49.4	76	3	AAZ44961	Aaz44961 P. alcali
37	38	49.4	77	3	AAZ44929	Aaz44929 P. alcali
38	38	49.4	79	3	AAZ44986	Aaz44986 P. alcali
39	37	48.1	52	3	AAZ44968	Aaz44968 P. alcali
40	33	42.9	76	3	AAZ44901	Aaz44901 P. alcali
41	33	42.9	76	3	AAZ44950	Aaz44950 P. alcali
42	29	37.7	87	3	AAZ44939	Aaz44939 P. alcali
43	29	37.7	87	3	AAZ44896	Aaz44896 P. alcali
44	28	36.4	73	3	AAZ88521	Aaz88521 P. alcali
45	28	36.4	75	3	AAZ44923	Aaz44923 P. alcali

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 05:21:44 ; Search time 63 Seconds
                                              (without alignments)
                                              868.742 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1022532

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
  c   1   14   18.2   37   2   US-08-379-057-10   Sequence 10, Appl
  c   2   13   16.9   42   2   US-08-875-154-25   Sequence 25, Appl
  c   3   13   16.9   44   2   US-08-875-154-28   Sequence 28, Appl
      4   13   16.9   45   2   US-08-875-154-16   Sequence 16, Appl
  c   5   13   16.9   45   2   US-08-875-154-17   Sequence 17, Appl
  c   6   13   16.9   97   1   US-08-479-783A-76   Sequence 76, Appl
  c   7   13   16.9   97   1   US-08-479-725-76   Sequence 76, Appl
  c   8   13   16.9   97   1   US-08-618-693-76   Sequence 76, Appl
  c   9   13   16.9   97   3   US-08-973-124-165   Sequence 165, App
  c 10   13   16.9   97   3   US-08-991-743C-76   Sequence 76, Appl
  c 11   13   16.9   97   4   US-09-851-486-76   Sequence 76, Appl
  c 12   13   16.9   97   5   PCT-US96-08014-165   Sequence 165, App

	13	12	15.6	15	1	US-08-182-968A-332	Sequence 332, App
	14	12	15.6	15	2	US-08-774-306A-332	Sequence 332, App
	15	12	15.6	15	3	US-09-064-156A-332	Sequence 332, App
	16	12	15.6	22	4	US-09-177-650-83	Sequence 83, Appl
	17	12	15.6	23	1	US-08-224-983-3	Sequence 3, Appli
	18	12	15.6	23	2	US-08-852-933-3	Sequence 3, Appli
	19	12	15.6	23	2	US-08-852-945-3	Sequence 3, Appli
	20	12	15.6	23	2	US-08-853-021-3	Sequence 3, Appli
	21	12	15.6	23	3	US-08-852-865-3	Sequence 3, Appli
c	22	12	15.6	40	1	US-08-040-548-55	Sequence 55, Appl
c	23	12	15.6	40	1	US-08-466-344-55	Sequence 55, Appl
c	24	12	15.6	42	3	US-09-549-853-21	Sequence 21, Appl
	25	12	15.6	53	4	US-08-956-171E-3413	Sequence 3413, Ap
	26	12	15.6	53	4	US-08-781-986A-3413	Sequence 3413, Ap
	27	12	15.6	54	4	US-09-213-052-3	Sequence 3, Appli
c	28	12	15.6	54	4	US-09-213-052-4	Sequence 4, Appli
c	29	12	15.6	67	4	US-09-513-999C-17478	Sequence 17478, A
	30	12	15.6	70	1	US-08-434-001-131	Sequence 131, App
	31	12	15.6	70	1	US-08-433-585-131	Sequence 131, App
	32	12	15.6	70	1	US-08-434-425-131	Sequence 131, App
	33	12	15.6	70	2	US-08-437-667-131	Sequence 131, App
c	34	12	15.6	70	2	US-08-894-578-114	Sequence 114, App
	35	12	15.6	70	3	US-08-906-955-131	Sequence 131, App
	36	12	15.6	70	3	US-08-945-909-131	Sequence 131, App
	37	12	15.6	70	3	US-09-396-002A-131	Sequence 131, App
	38	12	15.6	70	4	US-10-077-319-131	Sequence 131, App
	39	12	15.6	70	5	PCT-US96-06060-131	Sequence 131, App
	40	12	15.6	82	4	US-09-513-999C-35076	Sequence 35076, A
c	41	12	15.6	91	4	US-09-513-999C-16283	Sequence 16283, A
	42	12	15.6	94	4	US-09-621-976-13958	Sequence 13958, A
	43	11	14.3	11	4	US-09-723-942-31	Sequence 31, Appl
	44	11	14.3	15	1	US-08-182-968A-331	Sequence 331, App
	45	11	14.3	15	1	US-08-182-968A-333	Sequence 333, App

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 05:58:14 ; Search time 242 Seconds
                                              (without alignments)
                                              1630.339 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: OLIGO_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 3407233 seqs, 2561960514 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2126116

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA:*
                   1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                   2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                   3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                   4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                   5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                   6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                   7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                   8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                   9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                   11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                   12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                   13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                   14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                   15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                   16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                   17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                   18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                   19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                   20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                   21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
            %

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	19	24.7	34	15	US-10-407-637-29	Sequence 29, Appl
c	2	13	16.9	25	15	US-10-098-263B-95573	Sequence 95573, A
c	3	13	16.9	25	15	US-10-098-263B-122128	Sequence 122128,
c	4	13	16.9	97	10	US-09-851-486-76	Sequence 76, Appl
c	5	13	16.9	97	15	US-10-223-666-165	Sequence 165, App
	6	12	15.6	15	9	US-09-504-231A-354	Sequence 354, App
	7	12	15.6	15	9	US-09-274-553D-354	Sequence 354, App
	8	12	15.6	17	10	US-09-740-332-1504	Sequence 1504, Ap
c	9	12	15.6	17	10	US-09-740-332-3051	Sequence 3051, Ap
	10	12	15.6	17	10	US-09-817-879-1504	Sequence 1504, Ap
c	11	12	15.6	17	10	US-09-817-879-3051	Sequence 3051, Ap
	12	12	15.6	17	17	US-10-669-841-4097	Sequence 4097, Ap
c	13	12	15.6	17	17	US-10-669-841-5644	Sequence 5644, Ap
	14	12	15.6	22	15	US-10-096-578-83	Sequence 83, Appl
c	15	12	15.6	22	15	US-10-313-669-240	Sequence 240, App
	16	12	15.6	22	15	US-10-032-585-5594	Sequence 5594, Ap
	17	12	15.6	23	14	US-10-147-354-12	Sequence 12, Appl
	18	12	15.6	23	15	US-10-147-329-12	Sequence 12, Appl
c	19	12	15.6	25	15	US-10-098-263B-33953	Sequence 33953, A
c	20	12	15.6	25	15	US-10-098-263B-59952	Sequence 59952, A
	21	12	15.6	25	15	US-10-098-263B-78024	Sequence 78024, A
	22	12	15.6	25	15	US-10-098-263B-78087	Sequence 78087, A
c	23	12	15.6	25	15	US-10-098-263B-88245	Sequence 88245, A
c	24	12	15.6	25	15	US-10-098-263B-122127	Sequence 122127,
	25	12	15.6	25	15	US-10-098-263B-127349	Sequence 127349,
	26	12	15.6	25	15	US-10-098-263B-128968	Sequence 128968,
c	27	12	15.6	31	15	US-10-156-306-3230	Sequence 3230, Ap
c	28	12	15.6	31	16	US-10-138-674-19043	Sequence 19043, A
c	29	12	15.6	31	17	US-10-287-949A-19043	Sequence 19043, A
	30	12	15.6	32	9	US-09-825-301-50	Sequence 50, Appl
	31	12	15.6	32	9	US-09-757-417-10	Sequence 10, Appl
	32	12	15.6	32	14	US-10-042-945-10	Sequence 10, Appl
	33	12	15.6	32	15	US-10-033-527-50	Sequence 50, Appl
	34	12	15.6	32	18	US-10-770-668-53	Sequence 53, Appl
	35	12	15.6	36	18	US-10-770-668-55	Sequence 55, Appl
	36	12	15.6	37	14	US-10-002-784A-20	Sequence 20, Appl
c	37	12	15.6	37	14	US-10-002-784A-21	Sequence 21, Appl
c	38	12	15.6	42	16	US-10-082-714-21	Sequence 21, Appl
	39	12	15.6	50	16	US-10-131-827-1507	Sequence 1507, Ap
	40	12	15.6	53	8	US-08-781-986A-3413	Sequence 3413, Ap
	41	12	15.6	53	16	US-10-329-624-3413	Sequence 3413, Ap
	42	12	15.6	54	14	US-10-061-979-3	Sequence 3, Appli
c	43	12	15.6	54	14	US-10-061-979-4	Sequence 4, Appli
	44	12	15.6	60	10	US-09-908-975-6734	Sequence 6734, Ap
c	45	12	15.6	60	10	US-09-908-975-12898	Sequence 12898, A

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 05:20:29 ; Search time 1633 Seconds
                                            (without alignments)
                                            1718.224 Million cell updates/sec

Title: US-09-701-626A-11
Perfect score: 77
Sequence: 1 acctaacaactggttcaagt..........cccttaaccaaacgttaggc 77

Scoring table: OLIGO_NUC
               Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size :   0

Total number of hits satisfying chosen parameters: 664238

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :   EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
c 1	14	18.2	93	4	BG075044	BG075044 H3142F04-
2	13	16.9	52	1	AA823097	AA823097 vw40f06.r
3	13	16.9	68	9	CL213924	CL213924 W204C06 G
c 4	13	16.9	75	1	AU259835	AU259835 AU259835
c 5	13	16.9	92	9	AB082041	AB082041 Drosophil
c 6	12	15.6	32	2	BF131807	BF131807 601820724
7	12	15.6	34	1	AA939151	AA939151 oq07e11.s
c 8	12	15.6	46	1	AI000352	AI000352 ov11d10.s
9	12	15.6	47	8	BZ665531	BZ665531 EY00954-3

	10	12	15.6	49	1	AI697225	AI697225	tq17d08.x
	11	12	15.6	49	9	BX661579	BX661579	Arabidops
c	12	12	15.6	50	1	AU106001	AU106001	AU106001
c	13	12	15.6	51	7	CN850199	CN850199	000917AAF
c	14	12	15.6	53	4	BM122774	BM122774	L0515A02-
	15	12	15.6	54	7	CR425327	CR425327	CR425327
c	16	12	15.6	58	4	BI493871	BI493871	df106a09.
c	17	12	15.6	59	9	CR275870	CR275870	Forward s
c	18	12	15.6	59	9	CG466079	CG466079	01S0579-0
	19	12	15.6	60	4	BG099767	BG099767	ux88f11.y
c	20	12	15.6	60	9	CG408854	CG408854	Ds547 Ds
	21	12	15.6	61	8	BZ661780	BZ661780	SALK_0252
c	22	12	15.6	62	9	CL246534	CL246534	01S0569-0
c	23	12	15.6	66	2	BF130886	BF130886	601819680
	24	12	15.6	66	8	AZ448881	AZ448881	1M0246A22
	25	12	15.6	66	9	BX661578	BX661578	Arabidops
c	26	12	15.6	67	9	BX960820	BX960820	Reverse s
	27	12	15.6	69	9	CG529593	CG529593	OST110251
c	28	12	15.6	72	9	CR397223	CR397223	Arabidops
c	29	12	15.6	73	6	CA584952	CA584952	LBD01486.
c	30	12	15.6	74	9	CG596771	CG596771	OST259386
	31	12	15.6	75	1	AA991974	AA991974	ot01b06.s
	32	12	15.6	77	8	BH811295	BH811295	SALK_0581
	33	12	15.6	78	2	AW250424	AW250424	2822310.3
	34	12	15.6	78	6	CD289266	CD289266	9_K1.abd
	35	12	15.6	78	8	AF149686	AF149686	AF149686
c	36	12	15.6	78	8	AZ921778	AZ921778	1006032C0
c	37	12	15.6	83	8	BZ378495	BZ378495	SALK_1081
c	38	12	15.6	85	8	AZ608291	AZ608291	1M0432M17
	39	12	15.6	87	9	CR397846	CR397846	Arabidops
	40	12	15.6	88	1	AA104061	AA104061	mp01d10.r
	41	12	15.6	88	9	CR397847	CR397847	Arabidops
c	42	12	15.6	89	8	BZ593785	BZ593785	SALK_0820
	43	12	15.6	90	9	AL943231	AL943231	Arabidops
	44	12	15.6	92	1	AA595539	AA595539	ni47a05.s
	45	12	15.6	92	9	AL946063	AL946063	Arabidops

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 823.508 Seconds
                                           (without alignments)
                                           2469.262 Million cell updates/sec

Title: US-09-701-626A-80
Perfect score: 43
Sequence: 1 taacaattggttcaagtcgt..........cttcgctcactgcgggaccg 43

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                     %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
        1   43   100.0   43 6   BD211356   BD211356 Method of
        2   43   100.0   78 6   BD211314   BD211314 Method of
        3   43   100.0   78 6   BD211323   BD211323 Method of

```
4      43  100.0   7300  6  BD211279              BD211279 Method of
5      43  100.0  42143  6  BD211280              BD211280 Method of
```

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 198.73 Seconds
                                             (without alignments)
                                             1135.840 Million cell updates/sec

Title: US-09-701-626A-80
Perfect score: 43
Sequence: 1 taacaattggttcaagtcgt..........cttcgctcactgcgggaccg 43

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   43   100.0   43 3   AAZ44969   Aaz44969 P. alcali
     2   43   100.0   78 3   AAZ44936   Aaz44936 P. alcali
     3   43   100.0   78 3   AAZ44927   Aaz44927 P. alcali
     4   43   100.0   7300 3   AAZ44982   Aaz44982 P. alcali
     5   43   100.0   7300 3   AAZ44983   Aaz44983 P. alcali

6   43 100.0 13382 3 AAZ44984   Aaz44984 P. alcali

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 42.1865 Seconds
                                             (without alignments)
                                             724.496 Million cell updates/sec

Title: US-09-701-626A-80
Perfect score: 43
Sequence: 1 taacaattggttcaagtcgt..........cttcgctcactgcgggaccg 43

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 172.814 Seconds
                                              (without alignments)
                                              1274.950 Million cell updates/sec

Title: US-09-701-626A-80
Perfect score: 43
Sequence: 1 taacaattggttcaagtcgt..........cttcgctcactgcgggaccg 43

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
        %

```
Result          Query
   No.   Score  Match Length DB  ID                        Description
-----------------------------------------------------------------------------

No matches found
```

Run on: October 22, 2004, 06:54:36 ; Search time 1764.05 Seconds
                                                (without alignments)
                                                888.247 Million cell updates/sec

Title: US-09-701-626A-80
Perfect score: 43
Sequence: 1 taacaattggttcaagtcgt..........cttcgctcactgcgggaccg 43

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                   1: gb_est1:*
                   2: gb_est2:*
                   3: gb_htc:*
                   4: gb_est3:*
                   5: gb_est4:*
                   6: gb_est5:*
                   7: gb_est6:*
                   8: gb_gss1:*
                   9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                          %
Result   Query
   No.   Score Match Length DB   ID   Description

   No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1764.05 secs

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 823.508 Seconds
                                              (without alignments)
                                              2469.262 Million cell updates/sec

Title: US-09-701-626A-81
Perfect score: 43
Sequence: 1 taactattcagtcaagcgga..........aaaccccgctgcgcggtctt 43

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                  10: gb_ro:*
                  11: gb_sts:*
                  12: gb_sy:*
                  13: gb_un:*
                  14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
      1   43 100.0   43 6   BD211357   BD211357 Method of
      2   43 100.0   72 6   BD211340   BD211340 Method of
      3   43 100.0   14143 6   BD211277   BD211277 Method of
      4   43 100.0   14143 6   BD211278   BD211278 Method of

```
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OM nucleic - nucleic search, using sw model

Run on:          October 22, 2004, 06:02:20 ; Search time 198.73 Seconds
                                             (without alignments)
                                             1135.840 Million cell updates/sec

Title:           US-09-701-626A-81
Perfect score:   43
Sequence:          1 taactattcagtcaagcgga..........aaaccccgctgcgcggtctt 43

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:      3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :       N_Geneseq_23Sep04:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	43	3	AAZ44970	Aaz44970 P. alcali
2	43	100.0	72	3	AAZ44953	Aaz44953 P. alcali
3	43	100.0	14143	3	AAZ44981	Aaz44981 P. alcali

Run on: October 22, 2004, 06:55:41 ; Search time 42.1865 Seconds
                                               (without alignments)
                                               724.496 Million cell updates/sec

Title: US-09-701-626A-81
Perfect score: 43
Sequence: 1 taactattcagtcaagcgga..........aaaccccgctgcgcggtctt 43

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 42.1865 secs

                         GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 172.814 Seconds
                                               (without alignments)
                                               1274.950 Million cell updates/sec

Title: US-09-701-626A-81

```
Perfect score:      43
Sequence:           1 taactattcagtcaagcgga..........aaaccccgctgcgcggtctt 43

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters:        0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        Published_Applications_NA:*
                  1:  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3:  /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4:  /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5:  /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6:  /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7:  /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8:  /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9:  /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10:  /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11:  /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15:  /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16:  /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17:  /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  19:  /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  20:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  21:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result              Query
   No.    Score  Match Length DB   ID                      Description
   -------------------------------------------------------------------------

 No matches found


Search completed: October 22, 2004, 14:10:43
Job time : 172.814 secs

                        GenCore version 5.1.6
```

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:54:36 ; Search time 1764.05 Seconds
                                              (without alignments)
                                              888.247 Million cell updates/sec

Title: ' US-09-701-626A-81
Perfect score: 43
Sequence: 1 taactattcagtcaagcgga..........aaaccccgctgcgcggtctt 43

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1764.05 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 823.508 Seconds
                                            (without alignments)
                                            2469.262 Million cell updates/sec

Title: US-09-701-626A-82
Perfect score: 43
Sequence: 1 taacaatgcgctcaactgcg..........acttcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
     1   43   100.0   43   6   BD211358   BD211358 Method of

Title: US-09-701-626A-82
Perfect score: 43
Sequence: 1 taacaatgcgctcaactgcg.........acttcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

| | | % | | | | | |
Result No.	Score	Query Match	Length	DB	ID		Description
1	43	100.0	43	3	AAZ44971		Aaz44971 P. alcali

Search completed: October 22, 2004, 07:28:21
Job time : 198.73 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 42.1865 Seconds
                                             (without alignments)
                                             724.496 Million cell updates/sec

Title: US-09-701-626A-82
Perfect score: 43
Sequence: 1 taacaatgcgctcaactgcg..........acttcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 42.1865 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 172.814 Seconds
                                            (without alignments)
                                            1274.950 Million cell updates/sec

Title: US-09-701-626A-82
Perfect score: 43
Sequence: 1 taacaatgcgctcaactgcg..........acttcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB   ID   Description

```
    -------------------------------------------------------------------------

    No matches found


Search completed: October 22, 2004, 14:10:43
Job time : 172.814 secs

                          GenCore version 5.1.6
                 Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         October 22, 2004, 06:54:36 ; Search time 1764.05 Seconds
                                             (without alignments)
                                             888.247 Million cell updates/sec

Title:          US-09-701-626A-82
Perfect score: 43
Sequence:       1 taacaatgcgctcaactgcg..........acttcgttcgctggacagcc 43

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :      EST:*
                1:  gb_est1:*
                2:  gb_est2:*
                3:  gb_htc:*
                4:  gb_est3:*
                5:  gb_est4:*
                6:  gb_est5:*
                7:  gb_est6:*
                8:  gb_gss1:*
                9:  gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result          Query
   No.   Score  Match Length DB   ID                          Description
     ----------------------------------------------------------------------------
```

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1764.05 secs

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:        October 22, 2004, 06:27:10 ; Search time 823.508 Seconds
                                           (without alignments)
                                           2469.262 Million cell updates/sec

Title:         US-09-701-626A-83
Perfect score: 43
Sequence:      1 taacaagtcgctcaactgcc..........cactcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:      1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :     GenEmbl:*
               1:  gb_ba:*
               2:  gb_htg:*
               3:  gb_in:*
               4:  gb_om:*
               5:  gb_ov:*
               6:  gb_pat:*
               7:  gb_ph:*
               8:  gb_pl:*
               9:  gb_pr:*
               10:  gb_ro:*
               11:  gb_sts:*
               12:  gb_sy:*
               13:  gb_un:*
               14:  gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
  No.    Score   Match  Length DB   ID                    Description
  ------------------------------------------------------------------------------
     1      43   100.0      43  6   BD211359              BD211359 Method of
```

Title: US-09-701-626A-83
Perfect score: 43
Sequence: 1 taacaagtcgctcaactgcc..........cactcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   43 100.0   43 3   AAZ44972   Aaz44972 P. alcali

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 42.1865 Seconds
                                              (without alignments)
                                              724.496 Million cell updates/sec

Title: US-09-701-626A-83
Perfect score: 43
Sequence: 1 taacaagtcgctcaactgcc..........cactcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 42.1865 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 172.814 Seconds
                                               (without alignments)
                                               1274.950 Million cell updates/sec

Title: US-09-701-626A-83
Perfect score: 43
Sequence: 1 taacaagtcgctcaactgcc..........cactcgttcgctggacagcc 43

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
              1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
              2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
              3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
              4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
              5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
              6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
              7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
              8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
              9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
             10:   /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
             11:   /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
             12:   /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
             13:   /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
             14:   /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
             15:   /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
             16:   /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
             17:   /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
             18:   /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
             19:   /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
             20:   /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
             21:   /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB   ID   Description

   No matches found

```
              GenCore version 5.1.6
                 Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:           October 22, 2004, 07:28:32 ; Search time 1482 Seconds
                                             (without alignments)
                                             606.278 Million cell updates/sec

Title:            US-09-701-626A-84
Perfect score:    19
Sequence:         1 gccccttaaccaaacgtta 19

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:       51

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        GenEmbl:*
                  1:  gb_ba:*
                  2:  gb_htg:*
                  3:  gb_in:*
                  4:  gb_om:*
                  5:  gb_ov:*
                  6:  gb_pat:*
                  7:  gb_ph:*
                  8:  gb_pl:*
                  9:  gb_pr:*
                  10:  gb_ro:*
                  11:  gb_sts:*
                  12:  gb_sy:*
                  13:  gb_un:*
                  14:  gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                       %
Result                 Query
   No.   Score  Match Length DB   ID                      Description
-----------------------------------------------------------------------------
        1     19  100.0     19   6   BD211360             BD211360 Method of
        2     19  100.0     31   6   BD211366             BD211366 Method of
        3     19  100.0     52   6   BD211355             BD211355 Method of
        4     19  100.0     64   6   BD211394             BD211394 Method of
```

5	19	100.0	74	6	BD211374	BD211374 Method of
6	19	100.0	75	6	BD211310	BD211310 Method of
7	19	100.0	76	6	BD211290	BD211290 Method of
8	19	100.0	76	6	BD211301	BD211301 Method of
9	19	100.0	76	6	BD211318	BD211318 Method of
10	19	100.0	76	6	BD211336	BD211336 Method of
11	19	100.0	76	6	BD211348	BD211348 Method of
12	19	100.0	77	6	BD211287	BD211287 Method of
13	19	100.0	77	6	BD211295	BD211295 Method of
14	19	100.0	77	6	BD211297	BD211297 Method of
15	19	100.0	77	6	BD211298	BD211298 Method of
16	19	100.0	77	6	BD211300	BD211300 Method of
17	19	100.0	77	6	BD211302	BD211302 Method of
18	19	100.0	77	6	BD211316	BD211316 Method of
19	19	100.0	77	6	BD211317	BD211317 Method of
20	19	100.0	77	6	BD211324	BD211324 Method of
21	19	100.0	77	6	BD211331	BD211331 Method of
22	19	100.0	77	6	BD211339	BD211339 Method of
23	19	100.0	77	6	BD211341	BD211341 Method of
24	19	100.0	77	6	BD211344	BD211344 Method of
25	19	100.0	77	6	BD211351	BD211351 Method of
26	19	100.0	77	6	BD211353	BD211353 Method of
27	19	100.0	77	6	BD211354	BD211354 Method of
28	19	100.0	77	6	BD211395	BD211395 Method of
29	19	100.0	77	6	BD211398	BD211398 Method of
30	19	100.0	78	6	BD211294	BD211294 Method of
31	19	100.0	78	6	BD211299	BD211299 Method of
32	19	100.0	78	6	BD211309	BD211309 Method of
33	19	100.0	78	6	BD211314	BD211314 Method of
34	19	100.0	78	6	BD211320	BD211320 Method of
35	19	100.0	78	6	BD211323	BD211323 Method of
36	19	100.0	78	6	BD211325	BD211325 Method of
37	19	100.0	78	6	BD211327	BD211327 Method of
38	19	100.0	78	6	BD211335	BD211335 Method of
39	19	100.0	78	6	BD211343	BD211343 Method of
40	19	100.0	78	6	BD211405	BD211405 Method of
41	19	100.0	78	6	BD211406	BD211406 Method of
42	19	100.0	79	6	BD211328	BD211328 Method of
43	19	100.0	5957	1	AY129392	AY129392 Pseudomon
44	19	100.0	7275	1	AY129393	AY129393 Pseudomon
45	19	100.0	7300	6	BD211279	BD211279 Method of
46	19	100.0	9581	1	PAE223604	AJ223604 Pseudomon
c 47	19	100.0	11456	1	AE015694	AE015694 Shewanell
48	19	100.0	14143	6	BD211277	BD211277 Method of
49	19	100.0	14143	6	BD211278	BD211278 Method of
50	19	100.0	18042	1	AY038186	AY038186 Pseudomon
51	19	100.0	42143	6	BD211280	BD211280 Method of

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OM nucleic - nucleic search, using sw model   •

Run on: October 22, 2004, 09:26:43 ; Search time 235 Seconds
                                        (without alignments)
                                        424.421 Million cell updates/sec

Title: US-09-701-626A-84
Perfect score: 19
Sequence: 1 gccccttaaccaaacgtta 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 54

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
       1   19 100.0   19   3   AAZ44973   Aaz44973 P. alcali
       2   19 100.0   31   3   AAZ44979   Aaz44979 P. alcali
       3   19 100.0   34 10   ADH19155   Adh19155 Single-st
       4   19 100.0   52   3   AAZ44968   Aaz44968 P. alcali
       5   19 100.0   74   3   AAZ88516   Aaz88516 P. alcali
       6   19 100.0   74   3   AAZ88520   Aaz88520 P. alcali

7	19	100.0	74	3	AAZ88503	Aaz88503 P. alcali
8	19	100.0	74	3	AAZ88505	Aaz88505 P. alcali
9	19	100.0	74	3	AAZ88509	Aaz88509 P. alcali
10	19	100.0	74	3	AAZ88511	Aaz88511 P. alcali
11	19	100.0	74	3	AAZ88515	Aaz88515 P. alcali
12	19	100.0	75	3	AAZ88508	Aaz88508 P. alcali
13	19	100.0	75	3	AAZ44923	Aaz44923 P. alcali
14	19	100.0	75	3	AAZ88514	Aaz88514 P. alcali
15	19	100.0	76	3	AAZ44961	Aaz44961 P. alcali
16	19	100.0	76	3	AAZ44903	Aaz44903 P. alcali
17	19	100.0	76	3	AAZ44931	Aaz44931 P. alcali
18	19	100.0	76	3	AAZ44914	Aaz44914 P. alcali
19	19	100.0	76	3	AAZ44949	Aaz44949 P. alcali
20	19	100.0	77	3	AAZ44908	Aaz44908 P. alcali
21	19	100.0	77	3	AAZ44900	Aaz44900 P. alcali
22	19	100.0	77	3	AAZ44952	Aaz44952 P. alcali
23	19	100.0	77	3	AAZ44937	Aaz44937 P. alcali
24	19	100.0	77	3	AAZ44930	Aaz44930 P. alcali
25	19	100.0	77	3	AAZ44910	Aaz44910 P. alcali
26	19	100.0	77	3	AAZ44987	Aaz44987 P. alcali
27	19	100.0	77	3	AAZ44990	Aaz44990 P. alcali
28	19	100.0	77	3	AAZ44913	Aaz44913 P. alcali
29	19	100.0	77	3	AAZ44954	Aaz44954 P. alcali
30	19	100.0	77	3	AAZ44964	Aaz44964 P. alcali
31	19	100.0	77	3	AAZ44944	Aaz44944 P. alcali
32	19	100.0	77	3	AAZ44957	Aaz44957 P. alcali
33	19	100.0	77	3	AAZ44967	Aaz44967 P. alcali
34	19	100.0	77	3	AAZ44915	Aaz44915 P. alcali
35	19	100.0	77.	3	AAZ44929	Aaz44929 P. alcali
36	19	100.0	77	3	AAZ44911	Aaz44911 P. alcali
37	19	100.0	77	3	AAZ44966	Aaz44966 P. alcali
38	19	100.0	78	3	AAZ44912	Aaz44912 P. alcali
39	19	100.0	78	3	AAZ44936	Aaz44936 P. alcali
40	19	100.0	78	3	AAZ44907	Aaz44907 P. alcali
41	19	100.0	78	3	AAZ44948	Aaz44948 P. alcali
42	19	100.0	78	3	AAZ44956	Aaz44956 P. alcali
43	19	100.0	78	3	AAZ44922	Aaz44922 P. alcali
44	19	100.0	78	3	AAZ44997	Aaz44997 P. alcali
45	19	100.0	78	3	AAZ44933	Aaz44933 P. alcali
46	19	100.0	78	3	AAZ44938	Aaz44938 P. alcali
47	19	100.0	78	3	AAZ44940	Aaz44940 P. alcali
48	19	100.0	78	3	AAZ44927	Aaz44927 P. alcali
49	19	100.0	79	3	AAZ44941	Aaz44941 P. alcali
50	19	100.0	79	3	AAZ44986	Aaz44986 P. alcali
51	19	100.0	7300	3	AAZ44982	Aaz44982 P. alcali
52	19	100.0	7300	3	AAZ44983	Aaz44983 P. alcali
53	19	100.0	13382	3	AAZ44984	Aaz44984 P. alcali
54	19	100.0	14143	3	AAZ44981	Aaz44981 P. alcali

OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 19:34:52 ; Search time 313.172 Seconds
                                         (without alignments)
                                         2629.598 Million cell updates/sec

Title: US-09-701-626A-84
Perfect score: 19
Sequence: 1 gccccttaaccaaacgtta 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1:   gb_ba:*
                 2:   gb_htg:*
                 3:   gb_in:*
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*
                 28: em_un:*

```
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	BD211360	BD211360 Method of
2	19	100.0	31	6	BD211366	BD211366 Method of
3	19	100.0	52	6	BD211355	BD211355 Method of
4	19	100.0	64	6	BD211394	BD211394 Method of
5	19	100.0	74	6	BD211374	BD211374 Method of
6	19	100.0	75	6	BD211310	BD211310 Method of
7	19	100.0	76	6	BD211290	BD211290 Method of
8	19	100.0	76	6	BD211301	BD211301 Method of
9	19	100.0	76	6	BD211318	BD211318 Method of
10	19	100.0	76	6	BD211336	BD211336 Method of
11	19	100.0	76	6	BD211348	BD211348 Method of
12	19	100.0	77	6	BD211287	BD211287 Method of
13	19	100.0	77	6	BD211295	BD211295 Method of
14	19	100.0	77	6	BD211297	BD211297 Method of
15	19	100.0	77	6	BD211298	BD211298 Method of
16	19	100.0	77	6	BD211300	BD211300 Method of
17	19	100.0	77	6	BD211302	BD211302 Method of
18	19	100.0	77	6	BD211316	BD211316 Method of
19	19	100.0	77	6	BD211317	BD211317 Method of
20	19	100.0	77	6	BD211324	BD211324 Method of
21	19	100.0	77	6	BD211331	BD211331 Method of
22	19	100.0	77	6	BD211339	BD211339 Method of
23	19	100.0	77	6	BD211341	BD211341 Method of
24	19	100.0	77	6	BD211344	BD211344 Method of
25	19	100.0	77	6	BD211351	BD211351 Method of
26	19	100.0	77	6	BD211353	BD211353 Method of
27	19	100.0	77	6	BD211354	BD211354 Method of
28	19	100.0	77	6	BD211395	BD211395 Method of
29	19	100.0	77	6	BD211398	BD211398 Method of
30	19	100.0	78	6	BD211294	BD211294 Method of
31	19	100.0	78	6	BD211299	BD211299 Method of
32	19	100.0	78	6	BD211309	BD211309 Method of
33	19	100.0	78	6	BD211314	BD211314 Method of
34	19	100.0	78	6	BD211320	BD211320 Method of

35	19	100.0	78	6	BD211323	BD211323 Method of
36	19	100.0	78	6	BD211325	BD211325 Method of
37	19	100.0	78	6	BD211327	BD211327 Method of
38	19	100.0	78	6	BD211335	BD211335 Method of
39	19	100.0	78	6	BD211343	BD211343 Method of
40	19	100.0	78	6	BD211405	BD211405 Method of
41	19	100.0	78	6	BD211406	BD211406 Method of
42	19	100.0	79	6	BD211328	BD211328 Method of
43	19	100.0	5957	1	AY129392	AY129392 Pseudomon
44	19	100.0	7275	1	AY129393	AY129393 Pseudomon
45	19	100.0	7300	6	BD211279	BD211279 Method of

```
Title:            US-09-701-626A-84
Perfect score:    19
Sequence:         1 gccccttaaccaaacgtta 19


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         3373863 seqs, 2124099041 residues


Total number of hits satisfying chosen parameters:      6747726


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        N_Geneseq_29Jan04:*
                  1:  geneseqn1980s:*
                  2:  geneseqn1990s:*
                  3:  geneseqn2000s:*
                  4:  geneseqn2001as:*
                  5:  geneseqn2001bs:*
                  6:  geneseqn2002s:*
                  7:  geneseqn2003as:*
                  8:  geneseqn2003bs:*
                  9:  geneseqn2003cs:*
                  10: geneseqn2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	3	AAZ44973	Aaz44973 P. alcali
2	19	100.0	31	3	AAZ44979	Aaz44979 P. alcali
3	19	100.0	52	3	AAZ44968	Aaz44968 P. alcali
4	19	100.0	74	3	AAZ88516	Aaz88516 P. alcali
5	19	100.0	74	3	AAZ88520	Aaz88520 P. alcali
6	19	100.0	74	3	AAZ88503	Aaz88503 P. alcali
7	19	100.0	74	3	AAZ88505	Aaz88505 P. alcali
8	19	100.0	74	3	AAZ88509	Aaz88509 P. alcali
9	19	100.0	74	3	AAZ88511	Aaz88511 P. alcali
10	19	100.0	74	3	AAZ88515	Aaz88515 P. alcali
11	19	100.0	75	3	AAZ88508	Aaz88508 P. alcali
12	19	100.0	75	3	AAZ44923	Aaz44923 P. alcali
13	19	100.0	75	3	AAZ88514	Aaz88514 P. alcali
14	19	100.0	76	3	AAZ44961	Aaz44961 P. alcali
15	19	100.0	76	3	AAZ44903	Aaz44903 P. alcali
16	19	100.0	76	3	AAZ44931	Aaz44931 P. alcali
17	19	100.0	76	3	AAZ44914	Aaz44914 P. alcali
18	19	100.0	76	3	AAZ44949	Aaz44949 P. alcali

19	19	100.0	77	3	AAZ44908	Aaz44908 P. alcali
20	19	100.0	77	3	AAZ44900	Aaz44900 P. alcali
21	19	100.0	77	3	AAZ44952	Aaz44952 P. alcali
22	19	100.0	77	3	AAZ44937	Aaz44937 P. alcali
23	19	100.0	77	3	AAZ44930	Aaz44930 P. alcali
24	19	100.0	77	3	AAZ44910	Aaz44910 P. alcali
25	19	100.0	77	3	AAZ44987	Aaz44987 P. alcali
26	19	100.0	77	3	AAZ44990	Aaz44990 P. alcali
27	19	100.0	77	3	AAZ44913	Aaz44913 P. alcali
28	19	100.0	77	3	AAZ44954	Aaz44954 P. alcali
29	19	100.0	77	3	AAZ44964	Aaz44964 P. alcali
30	19	100.0	77	3	AAZ44944	Aaz44944 P. alcali
31	19	100.0	77	3	AAZ44957	Aaz44957 P. alcali
32	19	100.0	77	3	AAZ44967	Aaz44967 P. alcali
33	19	100.0	77	3	AAZ44915	Aaz44915 P. alcali
34	19	100.0	77	3	AAZ44929	Aaz44929 P. alcali
35	19	100.0	77	3	AAZ44911	Aaz44911 P. alcali
36	19	100.0	77	3	AAZ44966	Aaz44966 P. alcali
37	19	100.0	78	3	AAZ44912	Aaz44912 P. alcali
38	19	100.0	78	3	AAZ44936	Aaz44936 P. alcali
39	19	100.0	78	3	AAZ44907	Aaz44907 P. alcali
40	19	100.0	78	3	AAZ44948	Aaz44948 P. alcali
41	19	100.0	78	3	AAZ44956	Aaz44956 P. alcali
42	19	100.0	78	3	AAZ44922	Aaz44922 P. alcali
43	19	100.0	78	3	AAZ44997	Aaz44997 P. alcali
44	19	100.0	78	3	AAZ44933	Aaz44933 P. alcali
45	19	100.0	78	3	AAZ44938	Aaz44938 P. alcali

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 20:14:57 ; Search time 27.3534 Seconds
                                         (without alignments)
                                         385.475 Million cell updates/sec

Title: US-09-701-626A-84
Perfect score: 19
Sequence: 1 gccccttaaccaaacgtta 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                      %
Result   Query
    No.   Score Match Length DB ID   Description
----
 c   1   15   78.9   2134 3   US-08-961-083-81   Sequence 81, Appl
 c   2   15   78.9   2134 4   US-09-536-784-81   Sequence 81, Appl
     3   15   78.9 15363 4   US-08-961-527-139   Sequence 139, App
 c   4   14.8   77.9   403 4   US-09-621-976-8212   Sequence 8212, Ap
 c   5   14.8   77.9   1814 1   US-08-720-899-5   Sequence 5, Appli
 c   6   14.8   77.9   1814 1   US-08-459-610-5   Sequence 5, Appli
 c   7   14.8   77.9   1814 2   US-08-343-804-5   Sequence 5, Appli
 c   8   14.8   77.9   1814 2   US-08-687-399-5   Sequence 5, Appli
 c   9   14.8   77.9   1814 2   US-08-600-908A-5   Sequence 5, Appli
 c 10   14.8   77.9   1814 3   US-08-683-838A-5   Sequence 5, Appli
 c 11   14.8   77.9   1814 3   US-09-182-859-5   Sequence 5, Appli
 c 12   14.8   77.9   1814 4   US-09-672-459-5   Sequence 5, Appli

c	13	14.8	77.9	1814	4	US-09-636-252A-5	Sequence 5, Appli
c	14	14.8	77.9	1814	4	US-10-186-042-5	Sequence 5, Appli
c	15	14.8	77.9	5609	4	US-09-313-677-14	Sequence 14, Appl
c	16	14.8	77.9	5609	4	US-09-313-677-15	Sequence 15, Appl
c	17	14.8	77.9	7026	4	US-09-313-677-20	Sequence 20, Appl
c	18	14.8	77.9	7344	4	US-09-313-677-16	Sequence 16, Appl
c	19	14.8	77.9	11298	1	US-07-869-933-31	Sequence 31, Appl
c	20	14.8	77.9	11298	1	US-08-201-879A-2	Sequence 2, Appli
c	21	14.8	77.9	11298	3	US-09-103-663-31	Sequence 31, Appl
c	22	14.4	75.8	320	4	US-08-956-171E-3025	Sequence 3025, Ap
c	23	14.4	75.8	2179	4	US-08-858-207A-37	Sequence 37, Appl
c	24	14.2	74.7	56	3	US-08-258-287B-30	Sequence 30, Appl
c	25	14.2	74.7	56	3	US-08-368-704C-30	Sequence 30, Appl
	26	14.2	74.7	280	4	US-09-313-294A-256	Sequence 256, App
c	27	14.2	74.7	572	4	US-09-621-976-16094	Sequence 16094, A
c	28	14.2	74.7	1423	4	US-09-484-970B-47	Sequence 47, Appl
	29	14.2	74.7	1881	4	US-09-485-717-1	Sequence 1, Appli
c	30	14.2	74.7	3362	4	US-09-620-312D-469	Sequence 469, App
	31	14.2	74.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	32	14	73.7	732	4	US-09-134-000C-701	Sequence 701, App
c	33	13.8	72.6	482	5	PCT-US94-04174-28	Sequence 28, Appl
c	34	13.8	72.6	515	3	US-08-444-818-57	Sequence 57, Appl
c	35	13.8	72.6	912	4	US-09-134-000C-464	Sequence 464, App
c	36	13.8	72.6	1512	1	US-07-853-985A-5	Sequence 5, Appli
c	37	13.8	72.6	1512	1	US-07-681-703B-5	Sequence 5, Appli
c	38	13.8	72.6	1512	1	US-08-184-236-5	Sequence 5, Appli
c	39	13.8	72.6	1512	2	US-08-407-410B-5	Sequence 5, Appli
c	40	13.8	72.6	1512	2	US-08-485-500-5	Sequence 5, Appli
c	41	13.8	72.6	1512	5	PCT-US91-02370-5	Sequence 5, Appli
c	42	13.8	72.6	1512	5	PCT-US94-04174-5	Sequence 5, Appli
c	43	13.8	72.6	1788	2	US-08-722-806A-1	Sequence 1, Appli
c	44	13.8	72.6	1788	3	US-09-337-028-1	Sequence 1, Appli
c	45	13.8	72.6	1788	4	US-09-597-877-1	Sequence 1, Appli

```
Title:          US-09-701-626A-84
Perfect score:  19
Sequence:       1 gccccttaaccaaacgtta 19


Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0


Searched:       2947324 seqs, 2269024515 residues


Total number of hits satisfying chosen parameters:      5894648


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :      Published_Applications_NA:*
                1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
                    %
Result            Query
   No.    Score  Match Length DB  ID                        Description
        -------------------------------------------------------------------------
        1      19  100.0     34  15  US-10-407-637-29          Sequence 29, Appl
c       2      17   89.5    446  13  US-10-424-599-105228      Sequence 105228,
        3    15.8   83.2    407  10  US-09-803-719-2176        Sequence 2176, Ap
c       4    15.4   81.1    225  10  US-09-764-891-2515        Sequence 2515, Ap
        5    15.4   81.1    318  13  US-10-282-122A-2854       Sequence 2854, Ap
c       6    15.4   81.1    573  10  US-09-764-891-9928        Sequence 9928, Ap
c       7    15.4   81.1    815   9  US-09-912-020-5         Sequence 5, Appli
        8    15.4   81.1   2826  13  US-10-424-599-95809       Sequence 95809, A
```

c	9	15.4	81.1	14537	13	US-10-221-714A-77	Sequence 77, Appl
c	10	15.4	81.1	19553	9	US-09-764-847-1425	Sequence 1425, Ap
c	11	15.4	81.1	19553	15	US-10-092-154-1425	Sequence 1425, Ap
	12	15	78.9	520	13	US-10-027-632-276570	Sequence 276570,
	13	15	78.9	520	16	US-10-027-632-276570	Sequence 276570,
c	14	15	78.9	2134	9	US-09-765-272-81	Sequence 81, Appl
c	15	15	78.9	6702	10	US-09-769-787-209	Sequence 209, App
	16	15	78.9	15363	13	US-10-158-844-139	Sequence 139, App
	17	14.8	77.9	192	13	US-10-424-599-112733	Sequence 112733,
c	18	14.8	77.9	389	13	US-10-424-599-125493	Sequence 125493,
c	19	14.8	77.9	453	9	US-09-728-445-778	Sequence 778, App
	20	14.8	77.9	472	13	US-10-424-599-31184	Sequence 31184, A
c	21	14.8	77.9	517	13	US-10-424-599-121591	Sequence 121591,
c	22	14.8	77.9	564	13	US-10-027-632-286460	Sequence 286460,
c	23	14.8	77.9	564	16	US-10-027-632-286460	Sequence 286460,
c	24	14.8	77.9	710	10	US-09-774-639-93	Sequence 93, Appl
c	25	14.8	77.9	710	10	US-09-969-730-14	Sequence 14, Appl
c	26	14.8	77.9	710	17	US-10-621-363-14	Sequence 14, Appl
c	27	14.8	77.9	733	13	US-10-027-632-110691	Sequence 110691,
c	28	14.8	77.9	733	16	US-10-027-632-110691	Sequence 110691,
	29	14.8	77.9	873	13	US-10-282-122A-28010	Sequence 28010, A
c	30	14.8	77.9	908	15	US-10-001-883-18	Sequence 18, Appl
	31	14.8	77.9	1363	15	US-10-017-161-851	Sequence 851, App
	32	14.8	77.9	1363	16	US-10-292-798-729	Sequence 729, App
c	33	14.8	77.9	1656	13	US-10-282-122A-9732	Sequence 9732, Ap
c	34	14.8	77.9	1814	13	US-10-644-187-5	Sequence 5, Appli
c	35	14.8	77.9	1814	15	US-10-184-771-5	Sequence 5, Appli
c	36	14.8	77.9	1814	15	US-10-186-042-5	Sequence 5, Appli
c	37	14.8	77.9	2049	13	US-10-425-114-24968	Sequence 24968, A
c	38	14.8	77.9	2299	13	US-10-225-066A-751	Sequence 751, App
c	39	14.8	77.9	2299	16	US-10-374-780A-117	Sequence 117, App
c	40	14.8	77.9	3738	9	US-09-070-927A-708	Sequence 708, App
c	41	14.8	77.9	5687	15	US-10-239-676-21	Sequence 21, Appl
c	42	14.8	77.9	5687	15	US-10-240-453-29	Sequence 29, Appl
c	43	14.8	77.9	6132	15	US-10-311-455-1963	Sequence 1963, Ap
c	44	14.8	77.9	6659	16	US-10-191-803-271	Sequence 271, App
c	45	14.8	77.9	7113	15	US-10-311-455-778	Sequence 778, App

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 20:21:03 ; Search time 1022.89 Seconds
                                          (without alignments)
                                          554.686 Million cell updates/sec

Title: US-09-701-626A-84
Perfect score: 19
Sequence: 1 gccccttaaccaaacgtta 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*
                 28: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	89.5	393	14	T83717	T83717 yd65g07.r1
2	16.4	86.3	489	28	BZ415723	BZ415723 if58f06.g
3	16.4	86.3	547	14	CD204974	CD204974 HS1_11_G0
c 4	16.4	86.3	650	28	BZ419704	BZ419704 if58a08.b
5	16.4	86.3	653	28	BZ415670	BZ415670 if58a08.g
c 6	16.4	86.3	666	12	BM496661	BM496661 IpCGBr2_4
7	16.4	86.3	680	29	CE148619	CE148619 tigr-gss-
8	16.4	86.3	774	29	CG450998	CG450998 OGTBP60TV
c 9	16.4	86.3	800	29	CC976356	CC976356 ZUAAC81TH
c 10	16.4	86.3	825	28	BZ091711	BZ091711 CH230-220
11	16.4	86.3	908	29	CG930754	CG930754 MBEMC19TR
12	16.4	86.3	991	29	CG369735	CG369735 OG2CJ31TV
13	16	84.2	210	9	AV327666	AV327666 AV327666
c 14	16	84.2	647	10	BB127276	BB127276 BB127276
15	16	84.2	705	13	BU955140	BU955140 AGENCOURT
16	16	84.2	761	28	BH922207	BH922207 odi89e07.
17	16	84.2	959	13	BU163074	BU163074 AGENCOURT
c 18	15.8	83.2	329	12	BM131309	BM131309 TgESTzya9
c 19	15.8	83.2	425	13	BU575958	BU575958 TgESTzyb9
20	15.8	83.2	431	13	BY633973	BY633973 BY633973
c 21	15.8	83.2	440	13	BU576044	BU576044 TgESTzyb9
c 22	15.8	83.2	451	14	CB369194	CB369194 TgESTzyg9
c 23	15.8	83.2	463	12	BM176704	BM176704 TgESTzya9
c 24	15.8	83.2	464	12	BM131441	BM131441 TgESTzya9
c 25	15.8	83.2	473	14	CB755435	CB755435 TgESTzyi0
c 26	15.8	83.2	477	13	BQ254023	BQ254023 PL Z87 P.
27	15.8	83.2	481	29	CC754348	CC754348 ZMMBBb013
c 28	15.8	83.2	489	14	CB411845	CB411845 TgESTzyh5
c 29	15.8	83.2	490	12	BM131505	BM131505 TgESTzya9
c 30	15.8	83.2	498	13	BU575696	BU575696 TgESTzyb8
c 31	15.8	83.2	537	13	BQ254021	BQ254021 PL S59 P.
c 32	15.8	83.2	541	14	CB369491	CB369491 TgESTzyg7
c 33	15.8	83.2	547	12	BM176601	BM176601 TgESTzya9
c 34	15.8	83.2	555	14	CB755424	CB755424 TgESTzyi0
c 35	15.8	83.2	557	14	CB411344	CB411344 TgESTzyh3
c 36	15.8	83.2	565	14	CB754833	CB754833 TgESTzyi1
c 37	15.8	83.2	568	14	CB751956	CB751956 TgESTzyh7
c 38	15.8	83.2	570	9	AA167870	AA167870 CpEST.031
c 39	15.8	83.2	571	14	CB831771	CB831771 NcEST3a54
c 40	15.8	83.2	575	13	BU790668	BU790668 TgESTzyb5
c 41	15.8	83.2	577	12	BM040393	BM040393 TgESTzya5
c 42	15.8	83.2	582	14	CD657979	CD657979 EtESTef60
c 43	15.8	83.2	585	13	BU790755	BU790755 TgESTzyb5
c 44	15.8	83.2	586	14	CB753706	CB753706 TgESTzyh9
c 45	15.8	83.2	587	14	CB369362	CB369362 TgESTzyg8

```
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OM nucleic - nucleic search, using sw model

Run on:          May 13, 2004, 19:34:52 ; Search time 329.655 Seconds
                                          (without alignments)
                                          2629.598 Million cell updates/sec

Title:          US-09-701-626A-85
Perfect score:  20
Sequence:       1 ccgagtgagcgaagcgagcg 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:       6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*
                 15:  em_ba:*
                 16:  em_fun:*
                 17:  em_hum:*
                 18:  em_in:*
                 19:  em_mu:*
                 20:  em_om:*
                 21:  em_or:*
                 22:  em_ov:*
                 23:  em_pat:*
                 24:  em_ph:*
                 25:  em_pl:*
                 26:  em_ro:*
                 27:  em_sts:*
                 28:  em_un:*
```

```
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	6	BD211361	BD211361 Method of
	2	20	100.0	33	6	BD211362	BD211362 Method of
c	3	20	100.0	76	6	BD211349	BD211349 Method of
c	4	20	100.0	77	6	BD211281	BD211281 Method of
c	5	20	100.0	77	6	BD211295	BD211295 Method of
c	6	20	100.0	77	6	BD211298	BD211298 Method of
c	7	20	100.0	77	6	BD211317	BD211317 Method of
c	8	20	100.0	77	6	BD211341	BD211341 Method of
c	9	20	100.0	78	6	BD211350	BD211350 Method of
c	10	20	100.0	78	6	BD211405	BD211405 Method of
c	11	20	100.0	78	6	BD211406	BD211406 Method of
c	12	20	100.0	14143	6	BD211277	BD211277 Method of
c	13	20	100.0	14143	6	BD211278	BD211278 Method of
c	14	20	100.0	18042	1	AY038186	AY038186 Pseudomon
c	15	20	100.0	42143	6	BD211280	BD211280 Method of
	16	18.4	92.0	33	6	BD211363	BD211363 Method of
c	17	18.4	92.0	74	6	BD211374	BD211374 Method of
c	18	18.4	92.0	76	6	BD211288	BD211288 Method of
c	19	18.4	92.0	76	6	BD211337	BD211337 Method of
c	20	18.4	92.0	76	6	BD211342	BD211342 Method of
c	21	18.4	92.0	77	6	BD211287	BD211287 Method of
c	22	18.4	92.0	77	6	BD211297	BD211297 Method of
c	23	18.4	92.0	77	6	BD211300	BD211300 Method of
c	24	18.4	92.0	77	6	BD211316	BD211316 Method of
c	25	18.4	92.0	77	6	BD211331	BD211331 Method of
c	26	18.4	92.0	77	6	BD211339	BD211339 Method of
c	27	18.4	92.0	77	6	BD211344	BD211344 Method of
c	28	18.4	92.0	77	6	BD211353	BD211353 Method of
c	29	18.4	92.0	77	6	BD211354	BD211354 Method of
c	30	18.4	92.0	77	6	BD211395	BD211395 Method of
c	31	18.4	92.0	77	6	BD211398	BD211398 Method of
c	32	18.4	92.0	78	6	BD211294	BD211294 Method of
c	33	18.4	92.0	78	6	BD211315	BD211315 Method of
c	34	18.4	92.0	78	6	BD211320	BD211320 Method of

c	35	18.4	92.0	87	6	BD211319	BD211319 Method of
c	36	18.4	92.0	87	6	BD211338	BD211338 Method of
c	37	18.4	92.0	88	6	BD211283	BD211283 Method of
c	38	18.4	92.0	88	6	BD211326	BD211326 Method of
c	39	18.4	92.0	7275	1	AY129393	AY129393 Pseudomon
c	40	18.4	92.0	7300	6	BD211279	BD211279 Method of
c	41	18.4	92.0	11014	1	MTPFZ1A	X68367 M.thermofor
c	42	18.4	92.0	13514	1	MTPFV1A	X68366 M.thermofor
c	43	17.4	87.0	24365	1	AE015934	AE015934 Staphyloc
	44	17.4	87.0	30201	1	AB125341	AB125341 Staphyloc
	45	17.4	87.0	156522	2	AC131447	AC131447 Strongylo

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 18:33:43 ; Search time 125.862 Seconds
                                            (without alignments)
                                            675.056 Million cell updates/sec

Title: US-09-701-626A-85
Perfect score: 20
Sequence: 1 ccgagtgagcgaagcgagcg 20

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002s:*
                   7: geneseqn2003as:*
                   8: geneseqn2003bs:*
                   9: geneseqn2003cs:*
                   10: geneseqn2004s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                               SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
       ----
       1   20   100.0   20 3   AAZ44974   Aaz44974 P. alcali
       2   20   100.0   33 3   AAZ44975   Aaz44975 P. alcali
   c   3   20   100.0   73 3   AAZ88521   Aaz88521 P. alcali
   c   4   20   100.0   76 3   AAZ44962   Aaz44962 P. alcali
   c   5   20   100.0   77 3   AAZ44908   Aaz44908 P. alcali
   c   6   20   100.0   77 3   AAZ44894   Aaz44894 P. alcali
   c   7   20   100.0   77 3   AAZ44930   Aaz44930 P. alcali
   c   8   20   100.0   77 3   AAZ44954   Aaz44954 P. alcali

c	9	20	100.0	77	3	AAZ44911	Aaz44911 P. alcali
c	10	20	100.0	78	3	AAZ44963	Aaz44963 P. alcali
c	11	20	100.0	78	3	AAZ44997	Aaz44997 P. alcali
c	12	20	100.0	13382	3	AAZ44984	Aaz44984 P. alcali
c	13	20	100.0	14143	3	AAZ44981	Aaz44981 P. alcali
	14	18.4	92.0	33	3	AAZ44976	Aaz44976 P. alcali
c	15	18.4	92.0	73	3	AAZ88513	Aaz88513 P. alcali
c	16	18.4	92.0	74	3	AAZ88516	Aaz88516 P. alcali
c	17	18.4	92.0	74	3	AAZ88520	Aaz88520 P. alcali
c	18	18.4	92.0	74	3	AAZ88503	Aaz88503 P. alcali
c	19	18.4	92.0	74	3	AAZ88505	Aaz88505 P. alcali
c	20	18.4	92.0	74	3	AAZ88511	Aaz88511 P. alcali
c	21	18.4	92.0	74	3	AAZ88515	Aaz88515 P. alcali
c	22	18.4	92.0	76	3	AAZ44901	Aaz44901 P. alcali
c	23	18.4	92.0	76	3	AAZ44955	Aaz44955 P. alcali
c	24	18.4	92.0	76	3	AAZ44950	Aaz44950 P. alcali
c	25	18.4	92.0	77	3	AAZ44900	Aaz44900 P. alcali
c	26	18.4	92.0	77	3	AAZ44952	Aaz44952 P. alcali
c	27	18.4	92.0	77	3	AAZ44910	Aaz44910 P. alcali
c	28	18.4	92.0	77	3	AAZ44987	Aaz44987 P. alcali
c	29	18.4	92.0	77	3	AAZ44990	Aaz44990 P. alcali
c	30	18.4	92.0	77	3	AAZ44913	Aaz44913 P. alcali
c	31	18.4	92.0	77	3	AAZ44944	Aaz44944 P. alcali
c	32	18.4	92.0	77	3	AAZ44957	Aaz44957 P. alcali
c	33	18.4	92.0	77	3	AAZ44967	Aaz44967 P. alcali
c	34	18.4	92.0	77	3	AAZ44929	Aaz44929 P. alcali
c	35	18.4	92.0	77	3	AAZ44966	Aaz44966 P. alcali
c	36	18.4	92.0	78	3	AAZ44907	Aaz44907 P. alcali
c	37	18.4	92.0	78	3	AAZ44933	Aaz44933 P. alcali
c	38	18.4	92.0	78	3	AAZ44928	Aaz44928 P. alcali
c	39	18.4	92.0	84	3	AAZ88510	Aaz88510 P. alcali
c	40	18.4	92.0	87	3	AAZ44939	Aaz44939 P. alcali
c	41	18.4	92.0	87	3	AAZ44951	Aaz44951 P. alcali
c	42	18.4	92.0	87	3	AAZ44896	Aaz44896 P. alcali
c	43	18.4	92.0	87	3	AAZ44932	Aaz44932 P. alcali
c	44	18.4	92.0	7300	3	AAZ44982	Aaz44982 P. alcali
c	45	18.4	92.0	7300	3	AAZ44983	Aaz44983 P. alcali

Title: US-09-701-626A-85
Perfect score: 20
Sequence: 1 ccgagtgagcgaagcgagcg 20

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.8	79.0	3168	4	US-09-221-017B-924	Sequence 924, App
	2	15.2	76.0	432	4	US-09-252-991A-15041	Sequence 15041, A
c	3	15.2	76.0	641	4	US-09-247-155-66	Sequence 66, Appl
c	4	15.2	76.0	783	4	US-09-252-991A-14448	Sequence 14448, A
	5	15.2	76.0	954	4	US-09-252-991A-15180	Sequence 15180, A
	6	15.2	76.0	1778	4	US-08-934-386-4	Sequence 4, Appli
	7	15.2	76.0	1835	4	US-09-216-393B-80	Sequence 80, Appl
c	8	15.2	76.0	3653	4	US-09-596-824-3	Sequence 3, Appli
c	9	15.2	76.0	3653	4	US-09-885-329-3	Sequence 3, Appli
c	10	15.2	76.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	11	15.2	76.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	12	14.8	74.0	277	4	US-09-621-976-205	Sequence 205, App
	13	14.8	74.0	1900	4	US-08-961-527-219	Sequence 219, App
	14	14.8	74.0	2089	4	US-09-291-922-25	Sequence 25, Appl
c	15	14.8	74.0	536165	4	US-09-214-808-1	Sequence 1, Appli
	16	14.8	74.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	17	14.8	74.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	18	14.4	72.0	283	4	US-09-621-976-8416	Sequence 8416, Ap
	19	14.4	72.0	341	4	US-08-956-171E-4453	Sequence 4453, Ap
	20	14.4	72.0	361	4	US-09-280-590A-34	Sequence 34, Appl

	21	14.4	72.0	361	4	US-09-892-398-34	Sequence 34, Appl
c	22	14.4	72.0	3135	4	US-09-252-991A-7924	Sequence 7924, Ap
	23	14.4	72.0	4320	2	US-08-472-534-4	Sequence 4, Appli
	24	14.4	72.0	4518	4	US-08-961-527-121	Sequence 121, App
c	25	14.2	71.0	45	2	US-08-875-154-16	Sequence 16, Appl
	26	14.2	71.0	45	2	US-08-875-154-17	Sequence 17, Appl
c	27	14.2	71.0	213	4	US-09-134-000C-132	Sequence 132, App
	28	14.2	71.0	662	4	US-09-071-035-203	Sequence 203, App
c	29	14.2	71.0	666	4	US-09-134-000C-131	Sequence 131, App
	30	14.2	71.0	810	4	US-09-252-991A-4912	Sequence 4912, Ap
	31	14.2	71.0	810	4	US-09-252-991A-7666	Sequence 7666, Ap
	32	14.2	71.0	888	4	US-09-071-035-201	Sequence 201, App
	33	14.2	71.0	1017	3	US-08-793-634B-6	Sequence 6, Appli
c	34	14.2	71.0	1077	4	US-09-252-991A-7892	Sequence 7892, Ap
c	35	14.2	71.0	1221	4	US-09-489-039A-2832	Sequence 2832, Ap
	36	14.2	71.0	1302	4	US-09-489-039A-6233	Sequence 6233, Ap
	37	14.2	71.0	1488	4	US-09-252-991A-4918	Sequence 4918, Ap
	38	14.2	71.0	1536	4	US-09-252-991A-13102	Sequence 13102, A
	39	14.2	71.0	1594	2	US-08-955-713-1	Sequence 1, Appli
	40	14.2	71.0	1629	4	US-09-489-039A-5851	Sequence 5851, Ap
	41	14.2	71.0	1650	4	US-09-252-991A-10150	Sequence 10150, A
c	42	14.2	71.0	1725	4	US-09-252-991A-9926	Sequence 9926, Ap
c	43	14.2	71.0	1884	4	US-09-489-039A-5611	Sequence 5611, Ap
	44	14.2	71.0	3171	4	US-09-252-991A-7591	Sequence 7591, Ap
c	45	14.2	71.0	3210	4	US-09-252-991A-7962	Sequence 7962, Ap

```
Title:          US-09-701-626A-85
Perfect score:  20
Sequence:       1 ccgagtgagcgaagcgagcg 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters:      5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA:*
                1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

                              SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	16.4	82.0	730	15	US-10-161-051-183	Sequence 183, App
	2	16.4	82.0	737	15	US-10-161-051-184	Sequence 184, App
c	3	15.8	79.0	147	9	US-09-923-876-3887	Sequence 3887, Ap
c	4	15.8	79.0	147	11	US-09-923-876-3887	Sequence 3887, Ap
	5	15.8	79.0	300	9	US-09-854-124-22	Sequence 22, Appl
	6	15.8	79.0	406	10	US-09-918-995-36006	Sequence 36006, A
	7	15.8	79.0	1000	13	US-10-412-699B-815	Sequence 815, App
	8	15.8	79.0	1000	15	US-10-278-173-53	Sequence 53, Appl
	9	15.8	79.0	1000	16	US-10-302-267-127	Sequence 127, App

	10	15.8	79.0	1808	15	US-10-106-698-1596	Sequence 1596, Ap
c	11	15.8	79.0	1995	13	US-10-425-114-2854	Sequence 2854, Ap
c	12	15.8	79.0	2038	13	US-10-297-880-6	Sequence 6, Appli
	13	15.8	79.0	2437	16	US-10-104-047-368	Sequence 368, App
	14	15.8	79.0	3168	13	US-10-194-163-924	Sequence 924, App
	15	15.8	79.0	3548	10	US-09-930-213-277	Sequence 277, App
	16	15.8	79.0	3548	16	US-10-159-563-230	Sequence 230, App
c	17	15.8	79.0	25801	15	US-10-181-319-13	Sequence 13, Appl
	18	15.8	79.0	37672	15	US-10-004-113-49	Sequence 49, Appl
	19	15.8	79.0	42811	16	US-10-085-117-37	Sequence 37, Appl
	20	15.4	77.0	598	13	US-10-424-599-38692	Sequence 38692, A
c	21	15.4	77.0	1829	13	US-10-424-599-2805	Sequence 2805, Ap
c	22	15.4	77.0	2670	16	US-10-369-493-27185	Sequence 27185, A
c	23	15.2	76.0	209	13	US-10-424-599-99696	Sequence 99696, A
c	24	15.2	76.0	256	13	US-10-424-599-52411	Sequence 52411, A
	25	15.2	76.0	259	13	US-10-424-599-111086	Sequence 111086,
c	26	15.2	76.0	412	10	US-09-764-891-277	Sequence 277, App
c	27	15.2	76.0	489	10	US-09-918-995-35544	Sequence 35544, A
	28	15.2	76.0	504	9	US-09-864-761-6888	Sequence 6888, Ap
	29	15.2	76.0	549	9	US-09-867-701-2972	Sequence 2972, Ap
c	30	15.2	76.0	641	10	US-09-903-190-66	Sequence 66, Appl
	31	15.2	76.0	696	9	US-09-738-626-3357	Sequence 3357, Ap
c	32	15.2	76.0	783	15	US-10-156-761-3005	Sequence 3005, Ap
c	33	15.2	76.0	822	13	US-10-027-632-138643	Sequence 138643,
c	34	15.2	76.0	822	16	US-10-027-632-138643	Sequence 138643,
c	35	15.2	76.0	849	13	US-10-282-122A-22805	Sequence 22805, A
c	36	15.2	76.0	864	13	US-10-282-122A-13300	Sequence 13300, A
	37	15.2	76.0	870	16	US-10-369-493-46587	Sequence 46587, A
	38	15.2	76.0	872	13	US-10-425-114-26053	Sequence 26053, A
c	39	15.2	76.0	927	13	US-10-425-114-26015	Sequence 26015, A
c	40	15.2	76.0	975	13	US-10-424-599-80493	Sequence 80493, A
c	41	15.2	76.0	1164	16	US-10-369-493-32142	Sequence 32142, A
	42	15.2	76.0	1351	9	US-09-964-899-30	Sequence 30, Appl
c	43	15.2	76.0	1422	9	US-09-738-626-3356	Sequence 3356, Ap
	44	15.2	76.0	1434	15	US-10-156-761-7349	Sequence 7349, Ap
c	45	15.2	76.0	1601	16	US-10-411-010-16	Sequence 16, Appl

```
Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:      55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:  em_estba:*
                 2:  em_esthum:*
                 3:  em_estin:*
                 4:  em_estmu:*
                 5:  em_estov:*
                 6:  em_estpl:*
                 7:  em_estro:*
                 8:  em_htc:*
                 9:  gb_est1:*
                10:  gb_est2:*
                11:  gb_htc:*
                12:  gb_est3:*
                13:  gb_est4:*
                14:  gb_est5:*
                15:  em_estfun:*
                16:  em_estom:*
                17:  em_gss_hum:*
                18:  em_gss_inv:*
                19:  em_gss_pln:*
                20:  em_gss_vrt:*
                21:  em_gss_fun:*
                22:  em_gss_mam:*
                23:  em_gss_mus:*
                24:  em_gss_pro:*
                25:  em_gss_rod:*
                26:  em_gss_phg:*
                27:  em_gss_vrl:*
                28:  gb_gss1:*
                29:  gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	95.0	511	28	AZ170008	AZ170008 SP_0115_A
2	18.4	92.0	1459	12	BG745247	BG745247 602723418
c 3	17.4	87.0	394	28	AZ196356	AZ196356 SP_1031_B

	4	17.4	87.0	395	28	BH805091	BH805091	1008065D1
c	5	17.4	87.0	422	28	AZ160258	AZ160258	SP_0065_B
	6	17.4	87.0	513	12	BI377195	BI377195	BFLG3_000
	7	17.4	87.0	521	28	BZ636171	BZ636171	OGAMF17TM
c	8	17.4	87.0	546	28	BZ636157	BZ636157	OGAMF17TC
	9	17.4	87.0	572	28	AZ190496	AZ190496	SP_1017_A
c	10	17.4	87.0	740	28	AZ185574	AZ185574	SP_1005_A
	11	17.4	87.0	740	28	AZ196280	AZ196280	SP_1031_B
	12	17.4	87.0	751	29	CC985828	CC985828	ZUAEQ96TV
	13	17.4	87.0	759	28	AZ189633	AZ189633	SP_1015_A
	14	17.4	87.0	811	28	AZ195046	AZ195046	SP_1029_A
c	15	17.4	87.0	823	28	AZ191830	AZ191830	SP_1020_A
	16	17.4	87.0	825	28	BH839256	BH839256	LMCR15001
c	17	17.4	87.0	848	29	CC982757	CC982757	ZUAAW63TH
c	18	17.4	87.0	871	28	BH127648	BH127648	G-1123 Ma
c	19	17.4	87.0	913	28	BZ701921	BZ701921	PUCEJ37TD
c	20	17.4	87.0	945	29	CG367083	CG367083	OG0FA40TV
	21	17.4	87.0	1532	10	BF693932	BF693932	602082508
	22	17	85.0	351	12	BJ189780	BJ189780	BJ189780
	23	17	85.0	410	9	AL965152	AL965152	AL965152
c	24	17	85.0	424	13	BQ162383	BQ162383	WHE0436_F
	25	17	85.0	427	12	BJ203078	BJ203078	BJ203078
c	26	17	85.0	526	28	AZ151255	AZ151255	SP_0049_A
	27	17	85.0	688	29	CNS035BI	AL228519	Tetraodon
c	28	16.8	84.0	379	13	CA109349	CA109349	SCSGHR107
c	29	16.8	84.0	383	29	CC931933	CC931933	ZMMBBc054
c	30	16.8	84.0	394	29	CC838316	CC838316	ZMMBBc049
	31	16.8	84.0	400	14	CA704913	CA704913	wdk1c.pk0
	32	16.8	84.0	449	28	AQ852734	AQ852734	LMAJFV1_1
	33	16.8	84.0	471	14	CF243500	CF243500	3530_1_21
c	34	16.8	84.0	497	28	BH293647	BH293647	CH230-30M
	35	16.8	84.0	639	29	AG166602	AG166602	Pan trogl
c	36	16.8	84.0	681	29	CG025543	CG025543	ZMMBBc056
c	37	16.8	84.0	703	28	CC461497	CC461497	ZMMBBc035
c	38	16.8	84.0	733	29	CC814629	CC814629	ZMMBBc051
c	39	16.8	84.0	752	28	CC460796	CC460796	ZMMBBc036
c	40	16.8	84.0	763	29	CG025807	CG025807	ZMMBBc056
	41	16.8	84.0	771	14	CF243846	CF243846	3530_1_24
	42	16.8	84.0	780	29	CG900303	CG900303	ZMMBBb050
c	43	16.8	84.0	852	29	CG390408	CG390408	ZMMBBc057
c	44	16.8	84.0	857	29	CG388577	CG388577	ZMMBBc056

```
GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          October 22, 2004, 06:27:10 ; Search time 631.995 Seconds
                                             (without alignments)
                                             2469.262 Million cell updates/sec

Title:           US-09-701-626A-86
Perfect score:   33
Sequence:        1 aaactcgagggtcccgagtgagcgaagcgagcg 33

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:      1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result          Query
  No.   Score  Match Length DB   ID                    Description
----------------------------------------------------------------------------
    1     33   100.0     33  6   BD211362              BD211362 Method of
```

```
Title:          US-09-701-626A-86
Perfect score:  33
Sequence:       1 aaactcgagggtcccgagtgagcgaagcgagcg 33

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:     1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :      N_Geneseq_23Sep04:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004s:*
```

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
----
    1   33   100.0   33 3   AAZ44975   Aaz44975 P. alcali

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 32.3757 Seconds
                                              (without alignments)
                                              724.496 Million cell updates/sec

Title: US-09-701-626A-86
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagtgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 32.3757 secs

                         GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Title: US-09-701-626A-86
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagtgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
         1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
         3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
         4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
         5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
         6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
         7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
         8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
        10:   /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
        11:   /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
        12:   /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
        13:   /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
        14:   /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
        15:   /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
        16:   /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        17:   /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        18:   /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
        19:   /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
        20:   /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
        21:   /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description

  No matches found

Search completed: October 22, 2004, 14:10:43

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 670.297 Seconds
                                             (without alignments)
                                             2469.262 Million cell updates/sec

Title: US-09-701-626A-91
Perfect score: 35
Sequence: 1 tgctctagacggccgcccgttagcttaatcgttag 35

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
   ----
     1   35 100.0   35 6   BD211367   BD211367 Method of

ALIGNMENTS

RESULT 1
BD211367
LOCUS   BD211367   35 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Method of finding restriction enzyme.
ACCESSION   BD211367
VERSION   BD211367.1 GI:33021137
KEYWORDS   JP 2002517260-A/91.
SOURCE   unidentified
  ORGANISM   unidentified
                unclassified.
REFERENCE   1 (bases 1 to 35)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE   Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 91 18-JUN-2002;
                NEW ENGLAND BIOLABS INC
COMMENT   OS   Unknown
                PN   JP 2002517260-A/91
                PD   18-JUN-2002
                PF   11-JUN-1999 JP 2000553622
                PR   12-JUN-1998 US   60/089086,12-JUN-1998 US   60/089101 PI
                ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
                C12Q1/68,C12N15/09,C12N15/00
                CC   Description of Unknown Organism: Synthetic Oligonucleotide CC
                        based on
                CC   Pseudomonas Alcaligenes NEB#585 (ATCC 55044)
                FH   Key   Location/Qualifiers
                FT   source   1. .35
                FT   /organism='Unknown'.
FEATURES   Location/Qualifiers
     source   1. .35
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match   100.0%; Score 35; DB 6; Length 35;
  Best Local Similarity   100.0%; Pred. No. 2.2e-05;
  Matches   35; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TGCTCTAGACGGCCGCCCGTTAGCTTAATCGTTAG 35
            |||||||||||||||||||||||||||||||||||
Db   1 TGCTCTAGACGGCCGCCCGTTAGCTTAATCGTTAG 35

Search completed: October 22, 2004, 09:26:36
Job time : 671.297 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 161.757 Seconds

Title: US-09-701-626A-91
Perfect score: 35
Sequence: 1 tgctctagacggccgcccgttagcttaatcgttag 35

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
     1   35   100.0   35   3   AAZ44980   Aaz44980 P. alcali

                                ALIGNMENTS

RESULT 1
AAZ44980
ID   AAZ44980 standard; DNA; 35 BP.
XX
AC   AAZ44980;
XX
DT   16-MAY-2000   (first entry)

CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. AAZ44894-Z44980 represent the
CC   Pseudomonas alcaligenes repeat (PAR) elements described in the method of
CC   the invention
XX
SQ   Sequence 35 BP; 6 A; 10 C; 9 G; 10 T; 0 U; 0 Other;

   Query Match   100.0%;   Score 35;   DB 3;   Length 35;
   Best Local Similarity   100.0%;   Pred. No. 2.1e-06;
   Matches   35; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TGCTCTAGACGGCCGCCCGTTAGCTTAATCGTTAG 35
              |||||||||||||||||||||||||||||||||||
Db   1 TGCTCTAGACGGCCGCCCGTTAGCTTAATCGTTAG 35

Search completed: October 22, 2004, 07:28:22
Job time : 161.757 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 34.3378 Seconds
                                              (without alignments)
                                              724.496 Million cell updates/sec

Title: US-09-701-626A-91
Perfect score: 35
Sequence: 1 tgctctagacggccgcccgttagcttaatcgttag 35

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 34.3378 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 140.662 Seconds
                                             (without alignments)
                                             1274.950 Million cell updates/sec

Title: US-09-701-626A-91
Perfect score: 35
Sequence: 1 tgctctagacggccgcccgttagcttaatcgttag 35

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                  SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description

```
--------------------------------------------------------------------------

No matches found


Search completed: October 22, 2004, 14:10:44
Job time : 140.662 secs


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OM nucleic - nucleic search, using sw model

Run on:          October 22, 2004, 06:54:36 ; Search time 1435.85 Seconds
                                              (without alignments)
                                              888.247 Million cell updates/sec

Title:           US-09-701-626A-91
Perfect score:   35
Sequence:        1 tgctctagacggccgcccgttagcttaatcgttag 35

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :       EST:*
                 1:  gb_est1:*
                 2:  gb_est2:*
                 3:  gb_htc:*
                 4:  gb_est3:*
                 5:  gb_est4:*
                 6:  gb_est5:*
                 7:  gb_est6:*
                 8:  gb_gss1:*
                 9:  gb_gss2:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                             SUMMARIES
                   %
Result          Query
   No.   Score  Match Length DB   ID                        Description
   --------------------------------------------------------------------------
```

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1435.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004   Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 593.692 Seconds
                                             (without alignments)
                                             2469.262 Million cell updates/sec

Title: US-09-701-626A-90
Perfect score: 31
Sequence: 1 tgctctagacggccccttaaccaaacgttag 31

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   31   100.0   31 6   BD211366   BD211366 Method of

RESULT 1
BD211366
LOCUS   BD211366   31 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Method of finding restriction enzyme.
ACCESSION   BD211366
VERSION   BD211366.1 GI:33021136
KEYWORDS   JP 2002517260-A/90.
SOURCE   unidentified
  ORGANISM   unidentified
                unclassified.
REFERENCE   1 (bases 1 to 31)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE   Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 90 18-JUN-2002;
                NEW ENGLAND BIOLABS INC
COMMENT   OS   Unknown
                PN   JP 2002517260-A/90
                PD   18-JUN-2002
                PF   11-JUN-1999 JP 2000553622
                PR   12-JUN-1998 US   60/089086,12-JUN-1998 US   60/089101 PI
                ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
                C12Q1/68,C12N15/09,C12N15/00
                CC   Description of Unknown Organism: Synthetic Oligonucleotide CC
                         based on
                CC   Pseudomonas Alcaligenes NEB#585 (ATCC 55044)
                FH   Key   Location/Qualifiers
                FT   source   1. .31
                FT   /organism='Unknown'.
FEATURES   Location/Qualifiers
     source   1. .31
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match   100.0%; Score 31; DB 6; Length 31;
  Best Local Similarity   100.0%; Pred. No. 0.00028;
  Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TGCTCTAGACGGCCCCTTAACCAAACGTTAG 31
          |||||||||||||||||||||||||||||||
Db   1 TGCTCTAGACGGCCCCTTAACCAAACGTTAG 31

Search completed: October 22, 2004, 09:26:35
Job time : 593.692 secs

                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 143.27 Seconds

Title: US-09-701-626A-90
Perfect score: 31
Sequence: 1 tgctctagacggcccccttaaccaaacgttag 31

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                       %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   31 100.0   31 3 AAZ44979   Aaz44979 P. alcali

                                    ALIGNMENTS

RESULT 1
AAZ44979
ID   AAZ44979 standard; DNA; 31 BP.
XX
AC   AAZ44979;
XX
DT   16-MAY-2000   (first entry)

CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. AAZ44894-Z44980 represent the
CC   Pseudomonas alcaligenes repeat (PAR) elements described in the method of
CC   the invention
XX
SQ   Sequence 31 BP; 8 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match   100.0%; Score 31; DB 3; Length 31;
  Best Local Similarity 100.0%; Pred. No. 0.00012;
  Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TGCTCTAGACGGCCCCTTAACCAAACGTTAG 31
            |||||||||||||||||||||||||||||||
Db   1 TGCTCTAGACGGCCCCTTAACCAAACGTTAG 31

Search completed: October 22, 2004, 07:28:22
Job time : 143.27 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 30.4135 Seconds
                                              (without alignments)
                                              724.496 Million cell updates/sec

Title: US-09-701-626A-90
Perfect score: 31
Sequence: 1 tgctctagacggccccttaaccaaacgttag 31

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 30.4135 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 124.586 Seconds
                                             (without alignments)
                                             1274.950 Million cell updates/sec

Title: US-09-701-626A-90
Perfect score: 31
Sequence: 1 tgctctagacggccccttaaccaaacgttag 31

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
        1:    /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
        2:    /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
        3:    /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
        4:    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
        5:    /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
        6:    /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
        7:    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
        8:    /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
        9:    /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
       10:    /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
       11:    /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
       12:    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
       13:    /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
       14:    /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
       15:    /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
       16:    /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
       17:    /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
       18:    /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
       19:    /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
       20:    /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
       21:    /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description

```
-------------------------------------------------------------------------


No matches found


Search completed: October 22, 2004, 14:10:44
Job time : 124.586 secs

                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:           October 22, 2004, 06:54:36 ; Search time 1271.75 Seconds
                                               (without alignments)
                                               888.247 Million cell updates/sec

Title:           US-09-701-626A-90
Perfect score:   31
Sequence:        1 tgctctagacggccccttaaccaaacgttag 31

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :       EST:*
                 1:  gb_est1:*
                 2:  gb_est2:*
                 3:  gb_htc:*
                 4:  gb_est3:*
                 5:  gb_est4:*
                 6:  gb_est5:*
                 7:  gb_est6:*
                 8:  gb_gss1:*
                 9:  gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result          Query
  No.   Score Match Length DB   ID                        Description
  -------------------------------------------------------------------------
```

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1271.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 631.995 Seconds
                                             (without alignments)
                                             2469.262 Million cell updates/sec

Title: US-09-701-626A-89
Perfect score: 33
Sequence: 1 aaactcgagaccgcgcagcggggtttgcgtccg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
     1   33   100.0   33 6   BD211365   BD211365 Method of

RESULT 1
BD211365
LOCUS   BD211365   33 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Method of finding restriction enzyme.
ACCESSION   BD211365
VERSION   BD211365.1 GI:33021135
KEYWORDS   JP 2002517260-A/89.
SOURCE   unidentified
  ORGANISM   unidentified
                unclassified.
REFERENCE   1 (bases 1 to 33)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE   Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 89 18-JUN-2002;
                NEW ENGLAND BIOLABS INC
COMMENT   OS   Unknown
                PN   JP 2002517260-A/89
                PD   18-JUN-2002
                PF   11-JUN-1999 JP 2000553622
                PR   12-JUN-1998 US   60/089086,12-JUN-1998 US   60/089101 PI
                ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
                C12Q1/68,C12N15/09,C12N15/00
                CC   Description of Unknown Organism: Synthetic Oligonucleotide CC
                         based on
                CC   Pseudomonas Alcaligenes NEB#585 (ATCC 55044)
                FH   Key   Location/Qualifiers
                FT   source   1. .33
                FT   /organism='Unknown'.
FEATURES   Location/Qualifiers
     source   1. .33
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match   100.0%; Score 33; DB 6; Length 33;
  Best Local Similarity   100.0%; Pred. No. 0.075;
  Matches   33; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAACTCGAGACCGCGCAGCGGGGTTTGCGTCCG 33
            |||||||||||||||||||||||||||||||||
Db   1 AAACTCGAGACCGCGCAGCGGGGTTTGCGTCCG 33

Search completed: October 22, 2004, 09:26:35
Job time : 631.995 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 152.514 Seconds

Title: US-09-701-626A-89
Perfect score: 33
Sequence: 1 aaactcgagaccgcgcagcggggtttgcgtccg 33

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   33   100.0   33   3   AAZ44978   Aaz44978 P. alcali

                                ALIGNMENTS

RESULT 1
AAZ44978
ID   AAZ44978 standard; DNA; 33 BP.
XX
AC   AAZ44978;
XX
DT   16-MAY-2000 (first entry)

CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. AAZ44894-Z44980 represent the
CC   Pseudomonas alcaligenes repeat (PAR) elements described in the method of
CC   the invention
XX
SQ   Sequence 33 BP; 6 A; 10 C; 12 G; 5 T; 0 U; 0 Other;

   Query Match   100.0%;   Score 33;   DB 3;   Length 33;
   Best Local Similarity   100.0%;   Pred. No. 0.00034;
   Matches   33; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAACTCGAGACCGCGCAGCGGGGTTTGCGTCCG 33
               |||||||||||||||||||||||||||||||||
Db   1 AAACTCGAGACCGCGCAGCGGGGTTTGCGTCCG 33

Search completed: October 22, 2004, 07:28:22
Job time : 152.514 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 32.3757 Seconds
                                              (without alignments)
                                              724.496 Million cell updates/sec

Title: US-09-701-626A-89
Perfect score: 33
Sequence: 1 aaactcgagaccgcgcagcggggtttgcgtccg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 32.3757 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 132.624 Seconds
                                                (without alignments)
                                                1274.950 Million cell updates/sec

Title: US-09-701-626A-89
Perfect score: 33
Sequence: 1 aaactcgagaccgcgcagcggggtttgcgtccg 33

Scoring table: IDENTITY_NUC
                     Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                     1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                     2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                     3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                     4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                     5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                     6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                     7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                     8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                     9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                     10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                     11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                     12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                     13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                     14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                     15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                     16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                     17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                     18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                     19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                     20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                     21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description

No matches found

Search completed: October 22, 2004, 14:10:44
Job time : 133.624 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:54:36 ; Search time 1353.8 Seconds
                                             (without alignments)
                                             888.247 Million cell updates/sec

Title: US-09-701-626A-89
Perfect score: 33
Sequence: 1 aaactcgagaccgcgcagcggggtttgcgtccg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1353.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 631.995 Seconds
                                          (without alignments)
                                          2469.262 Million cell updates/sec

Title: US-09-701-626A-88
Perfect score: 33
Sequence: 1 aaactcgaggctgtccagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
               1: gb_ba:*
               2: gb_htg:*
               3: gb_in:*
               4: gb_om:*
               5: gb_ov:*
               6: gb_pat:*
               7: gb_ph:*
               8: gb_pl:*
               9: gb_pr:*
               10: gb_ro:*
               11: gb_sts:*
               12: gb_sy:*
               13: gb_un:*
               14: gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
      1   33   100.0   33   6   BD211364   BD211364 Method of

RESULT 1
BD211364
LOCUS   BD211364   33 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Method of finding restriction enzyme.
ACCESSION   BD211364
VERSION   BD211364.1 GI:33021134
KEYWORDS   JP 2002517260-A/88.
SOURCE   unidentified
  ORGANISM   unidentified
               unclassified.
REFERENCE   1 (bases 1 to 33)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE   Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 88 18-JUN-2002;
               NEW ENGLAND BIOLABS INC
COMMENT   OS   Unknown
               PN   JP 2002517260-A/88
               PD   18-JUN-2002
               PF   11-JUN-1999 JP 2000553622
               PR   12-JUN-1998 US   60/089086,12-JUN-1998 US   60/089101 PI
               ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
               C12Q1/68,C12N15/09,C12N15/00
               CC   Description of Unknown Organism: Synthetic Oligonucleotide CC
                       based on
               CC   Pseudomonas Alcaligenes NEB#585 (ATCC 55044)
               FH   Key   Location/Qualifiers
               FT   source   1. .33
               FT   /organism='Unknown'.
FEATURES   Location/Qualifiers
     source   1. .33
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match   100.0%;   Score 33; DB 6; Length 33;
  Best Local Similarity   100.0%;   Pred. No. 0.0084;
  Matches   33; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAACTCGAGGCTGTCCAGCGAGCGAAGCGAGCG 33
            |||||||||||||||||||||||||||||||||
Db   1 AAACTCGAGGCTGTCCAGCGAGCGAAGCGAGCG 33

Search completed: October 22, 2004, 09:26:35
Job time : 631.995 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 152.514 Seconds

Title: US-09-701-626A-88
Perfect score: 33
Sequence: 1 aaactcgaggctgtccagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
   ----
     1   33 100.0   33   3   AAZ44977   Aaz44977 P. alcali

                              ALIGNMENTS

RESULT 1
AAZ44977
ID   AAZ44977 standard; DNA; 33 BP.
XX
AC   AAZ44977;
XX
DT   16-MAY-2000   (first entry)

CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. AAZ44894-Z44980 represent the
CC   Pseudomonas alcaligenes repeat (PAR) elements described in the method of
CC   the invention
XX
SQ   Sequence 33 BP; 9 A; 9 C; 12 G; 3 T; 0 U; 0 Other;

      Query Match   100.0%;   Score 33; DB 3; Length 33;
      Best Local Similarity   100.0%;   Pred. No. 0.0004;
      Matches   33; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAACTCGAGGCTGTCCAGCGAGCGAAGCGAGCG 33
                |||||||||||||||||||||||||||||||||
Db   1 AAACTCGAGGCTGTCCAGCGAGCGAAGCGAGCG 33

Search completed: October 22, 2004, 07:28:22
Job time : 153.514 secs

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 32.3757 Seconds
                                            (without alignments)
                                            724.496 Million cell updates/sec

Title: US-09-701-626A-88
Perfect score: 33
Sequence: 1 aaactcgaggctgtccagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 32.3757 secs

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 132.624 Seconds
                                              (without alignments)
                                              1274.950 Million cell updates/sec

Title: US-09-701-626A-88
Perfect score: 33
Sequence: 1 aaactcgaggctgtccagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                   1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                   2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                   3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                   4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                   5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                   6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                   7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                   8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                   9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                   11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                   12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                   13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                   14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                   15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                   16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                   17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                   18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                   19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                   20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                   21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 14:10:43
Job time : 132.624 secs

                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:54:36 ; Search time 1353.8 Seconds
                                              (without alignments)
                                              888.247 Million cell updates/sec

Title: US-09-701-626A-88
Perfect score: 33
Sequence: 1 aaactcgaggctgtccagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1353.8 secs

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:27:10 ; Search time 631.995 Seconds
                                             (without alignments)
                                             2469.262 Million cell updates/sec

Title: US-09-701-626A-87
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	33	6	BD211363	BD211363 Method of

RESULT 1
BD211363
```
LOCUS        BD211363                33 bp    DNA      linear    PAT 17-JUL-2003
DEFINITION   Method of finding restriction enzyme.
ACCESSION    BD211363
VERSION      BD211363.1  GI:33021133
KEYWORDS     JP 2002517260-A/87.
SOURCE       unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE    1  (bases 1 to 33)
  AUTHORS    Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE      Method of finding restriction enzyme
  JOURNAL    Patent: JP 2002517260-A 87 18-JUN-2002;
             NEW ENGLAND BIOLABS INC
COMMENT      OS   Unknown
             PN   JP 2002517260-A/87
             PD   18-JUN-2002
             PF   11-JUN-1999 JP 2000553622
             PR   12-JUN-1998 US     60/089086,12-JUN-1998 US     60/089101 PI
             ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
             C12Q1/68,C12N15/09,C12N15/00
             CC   Description of Unknown Organism: Synthetic Oligonucleotide  CC
                     based on
             CC   Pseudomonas Alcaligenes NEB#585 (ATCC 55044)
             FH   Key              Location/Qualifiers
             FT   source           1. .33
             FT                    /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN
```

```
  Query Match            100.0%;  Score 33;  DB 6;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 0.03;
  Matches   33;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy       1 AAACTCGAGGGTCCCGAGCGAGCGAAGCGAGCG 33
           |||||||||||||||||||||||||||||||||
Db       1 AAACTCGAGGGTCCCGAGCGAGCGAAGCGAGCG 33
```

Search completed: October 22, 2004, 09:26:35
Job time : 632.995 secs

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:02:20 ; Search time 152.514 Seconds

Title: US-09-701-626A-87
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_23Sep04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB ID   Description
  ----
    1   33   100.0   33   3 AAZ44976   Aaz44976 P. alcali

                                ALIGNMENTS

RESULT 1
AAZ44976
ID   AAZ44976 standard; DNA; 33 BP.
XX
AC   AAZ44976;
XX
DT   16-MAY-2000   (first entry)

Search completed: October 22, 2004, 07:28:21
Job time : 152.514 secs

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:55:41 ; Search time 32.3757 Seconds
                                            (without alignments)
                                            724.496 Million cell updates/sec

Title: US-09-701-626A-87
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                          %
Result   Query
  No.   Score Match Length DB   ID   Description

 No matches found

Search completed: October 22, 2004, 13:45:50
Job time : 32.3757 secs

OM nucleic - nucleic search, using sw model

Run on: October 22, 2004, 06:59:51 ; Search time 132.624 Seconds
                                              (without alignments)
                                              1274.950 Million cell updates/sec

Title: US-09-701-626A-87
Perfect score: 33
Sequence: 1 aaactcgagggtcccgagcgagcgaagcgagcg 33

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
                   1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                   2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                   3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                   4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                   5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                   6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                   7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                   8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                   9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                   11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                   12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                   13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                   14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                   15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                   16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                   17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                   18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                   19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                   20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                   21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description

```
        ----------------------------------------------------------------------

   No matches found


   Search completed: October 22, 2004, 14:10:43
   Job time : 132.624 secs


                               GenCore version 5.1.6
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   OM nucleic - nucleic search, using sw model

   Run on:        October 22, 2004, 06:54:36 ; Search time 1353.8 Seconds
                                               (without alignments)
                                               888.247 Million cell updates/sec

   Title:         US-09-701-626A-87
   Perfect score: 33
   Sequence:      1 aaactcgagggtcccgagcgagcgaagcgagcg 33


   Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


   Searched:      32822875 seqs, 18219865908 residues


   Total number of hits satisfying chosen parameters:      0

   Minimum DB seq length: 0
   Maximum DB seq length: 2000000000

   Post-processing: Minimum Match 100%
                    Maximum Match 100%
                    Listing first 1000 summaries


   Database :     EST:*
                  1:  gb_est1:*
                  2:  gb_est2:*
                  3:  gb_htc:*
                  4:  gb_est3:*
                  5:  gb_est4:*
                  6:  gb_est5:*
                  7:  gb_est6:*
                  8:  gb_gss1:*
                  9:  gb_gss2:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                       %
   Result          Query
     No.   Score  Match Length DB  ID                    Description
        ----------------------------------------------------------------------
```

No matches found

Search completed: October 22, 2004, 13:39:40
Job time : 1353.8 secs

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _70 %_

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.